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OM protein - protein search, using sw model
Run on: September 10, 2005, 01:09:25 ; Search time 480 Seconds
(without alignments)
12.167 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LNWFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 59692

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	26	100.0	5	33	US-10-795-795-12	Sequence 12, Appl
2	20	76.9	5	27	US-10-111-983-33494	Sequence 33494, A
3	19	73.1	5	30	US-10-436-549-13	Sequence 13, Appl
4	19	73.1	5	33	US-10-712-425-13	Sequence 13, Appl
5	19	73.1	5	33	US-10-773-032-13	Sequence 13, Appl
6	19	73.1	5	34	US-10-807-807-2261	Sequence 2261, Ap
7	19	73.1	5	34	US-10-807-807A-2261	Sequence 2261, Ap
8	19	73.1	5	34	US-10-808-121-2261	Sequence 2261, Ap
9	19	73.1	5	34	US-10-808-121A-2261	Sequence 2261, Ap
10	19	73.1	5	34	US-10-808-187-2261	Sequence 2261, Ap
11	19	73.1	5	34	US-10-808-187A-2261	Sequence 2261, Ap
12	19	73.1	5	34	US-10-852-357-2255	Sequence 2255, Ap
13	18	69.2	5	23	US-09-855-604-905	Sequence 905, App
14	18	69.2	5	23	US-09-855-604A-905	Sequence 905, App
15	17	65.4	5	27	US-10-111-983-7056	Sequence 7056, Ap
16	17	65.4	5	27	US-10-111-983-20387	Sequence 20387, A
17	17	65.4	5	27	US-10-111-983-32648	Sequence 32648, A
18	16	61.5	5	1	PCT-US00-42030A-5	Sequence 5, Appli
19	16	61.5	5	1	PCT-US02-39109-4	Sequence 4, Appli
20	16	61.5	5	1	PCT-US94-11907-20	Sequence 20, Appl
21	16	61.5	5	1	PCT-US94-11907-31	Sequence 31, Appl
22	16	61.5	5	1	PCT-US98-03908-27	Sequence 27, Appl
23	16	61.5	5	3	US-07-864-452-146	Sequence 146, App
24	16	61.5	5	3	US-07-864-452A-146	Sequence 146, App
25	16	61.5	5	3	US-07-920-136A-12	Sequence 12, Appl
26	16	61.5	5	3	US-07-944-882-26	Sequence 26, Appl
27	16	61.5	5	3	US-07-987-674-5	Sequence 5, Appli
28	16	61.5	5	4	US-08-067-523-4	Sequence 4, Appli
29	16	61.5	5	5	US-08-107-777-5	Sequence 5, Appli
30	16	61.5	5	5	US-08-233-619-20	Sequence 20, Appl
31	16	61.5	5	6	US-08-233-619-31	Sequence 31, Appl
32	16	61.5	5	8	US-08-418-928-146	Sequence 146, App
33	16	61.5	5	12	US-08-850-127-27	Sequence 27, Appl
34	16	61.5	5	17	US-09-334-513-4	Sequence 4, Appli
35	16	61.5	5	17	US-09-344-406-12	Sequence 12, Appl
36	16	61.5	5	19	US-09-563-736-12	Sequence 12, Appl
37	16	61.5	5	21	US-09-709-241-5	Sequence 5, Appli
38	16	61.5	5	24	US-09-943-944E-27	Sequence 27, Appl
39	16	61.5	5	26	US-10-006-869-242	Sequence 242, App
40	16	61.5	5	26	US-10-006-869-1725	Sequence 1725, App
41	16	61.5	5	26	US-10-031-289-647	Sequence 647, App
42	16	61.5	5	26	US-10-031-289-897	Sequence 897, App
43	16	61.5	5	27	US-10-111-983-2485	Sequence 2485, Ap
44	16	61.5	5	27	US-10-111-983-6325	Sequence 6325, Ap
45	16	61.5	5	27	US-10-111-983-11986	Sequence 11986, A

ALIGNMENTS

RESULT 1
US-10-795-795-12
; Sequence 12, Application US/10795795
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-795-795-12

Query Match 100.0%; Score 26; DB 33; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNFS 5
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Db 1 LDNFS 5

RESULT 2

US-10-111-983-33494

; Sequence 33494, Application US/10111983

; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA

; APPLICANT: GALEOTTI Cesira

; APPLICANT: GRANDI Guido

; APPLICANT: MASIGNANI Vega

; APPLICANT: MORA Mariarosa

; APPLICANT: PIZZA Mariagrazia

; APPLICANT: RAPPUOLI Rino

; APPLICANT: RATTI Giulio

; APPLICANT: SCARLATO Vincenzo

; APPLICANT: SCARSELLI Maria

; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES

; FILE REFERENCE: 2300-1654 (PP01654.003)

; CURRENT APPLICATION NUMBER: US/10/111.983

; CURRENT FILING DATE: 2003-06-27

; PRIOR APPLICATION NUMBER: US-60/162616

; PRIOR FILING DATE: 1999-10-29

; NUMBER OF SEQ ID NOS: 37764

; SOFTWARE: SeqWin99, version 1.02

; SEQ ID NO 33494

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Neisseria

US-10-111-983-33494

Query Match 76.9%; Score 20; DB 27; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
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Db 1 IDNF 4

RESULT 3

US-10-436-549-13

; Sequence 13, Application US/10436549

; GENERAL INFORMATION:

; APPLICANT: Lee, Frank D.

; APPLICANT: Meng, Dr. Xun

; APPLICANT: Chan, John W.

; APPLICANT: Zhang, Shengsheng

; APPLICANT: Benkovic, Stephen J.

; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN

; FILE REFERENCE: ENGE-P01-001

; CURRENT APPLICATION NUMBER: US/10/436.549

; CURRENT FILING DATE: 2003-05-12

; PRIOR APPLICATION NUMBER: 60/379,626

; PRIOR FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: 60/393,233

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,235

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,211

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,280

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,197

; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/433,319
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 614
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-10-436-549-13

Query Match 73.1%; Score 19; DB 30; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
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Db 1 DNFN 4

RESULT 4

US-10-712-425-13

; Sequence 13, Application US/10712425

; GENERAL INFORMATION:

; APPLICANT: LEE, FRANK D.

; APPLICANT: MENG, XUN

; APPLICANT: LIVINGSTON, DAVID

; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN

; FILE REFERENCE: ENGE-P02-001

; CURRENT APPLICATION NUMBER: US/10/712.425

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/379,626

; PRIOR FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: 60/393,137

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,197

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,211

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,223

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,233

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,235

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/393,280

; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/430,948

; PRIOR FILING DATE: 2002-12-04

; PRIOR APPLICATION NUMBER: 60/433,319

; PRIOR FILING DATE: 2002-12-13

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-712-425-13

Query Match 73.1%; Score 19; DB 33; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
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Db 1 DNFN 4

RESULT 5
US-10-773-032-13
; Sequence 13, Application US/10773032
; GENERAL INFORMATION:
; APPLICANT: LEE, FRANK D.
; APPLICANT: MENG, XUN
; APPLICANT: AFEYAN, NOUBAR B.
; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN
; MODIFICATION ANALYSIS
; FILE REFERENCE: ENGE-P03-001
; CURRENT APPLICATION NUMBER: US/10/773,032
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: 10/712,425
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/436,549
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,626
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,197
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-773-032-13

Query Match 73.1%; Score 19; DB 33; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
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Db 1 DNFN 4

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US-10-807-807-2261
; Sequence 2261, Application US/10807807
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory syndrome virus
US-10-807-807A-2261

; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-2261

Query Match 73.1%; Score 19; DB 34; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
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Db 2 DNFA 5

RESULT 7
US-10-807-807A-2261
; Sequence 2261, Application US/10807807A
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807A
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory syndrome virus
US-10-807-807A-2261

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Query Match      73.1%; Score 19; DB 34; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
Db 2 DNFA 5

RESULT 8
US-10-808-121-2261
; Sequence 2261, Application US/10808121
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: NOVEL HUMAN VIRUS CAUSING SEVERE ACUTE RESPIRATORY SYNDROME
; FILE REFERENCE: V9661.0069
; CURRENT APPLICATION NUMBER: US/10/808,121
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 2470
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-121-2261

Query Match      73.1%; Score 19; DB 34; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
Db 2 DNFA 5

RESULT 9
US-10-808-121A-2261
; Sequence 2261, Application US/10808121A
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: NOVEL HUMAN VIRUS CAUSING SEVERE ACUTE RESPIRATORY SYNDROME
; FILE REFERENCE: V9661.0069
; CURRENT APPLICATION NUMBER: US/10/808,121A
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
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; PRIOR APPLICATION NUMBER: 60/459,931
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; PRIOR FILING DATE: 2003-04-02
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; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 2470
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory syndrome virus
US-10-808-121A-2261

Query Match      73.1%; Score 19; DB 34; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
Db 2 DNFA 5

RESULT 10
US-10-808-187-2261
; Sequence 2261, Application US/10808187
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-2261

Query Match      73.1%; Score 19; DB 34; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
Db 2 DNFA 5
```

```
RESULT 11
US-10-808-187A-2261
; Sequence 2261, Application US/10808187A
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187A
; CURRENT FILING DATE: 2004-03-24
; PRIOR FILING DATE: 2003-03-24
; PRIOR FILING DATE: 2003-03-24
; PRIOR FILING DATE: 2003-03-24
; PRIOR FILING DATE: 2003-03-26
; PRIOR FILING DATE: 2003-03-26
; PRIOR FILING DATE: 2003-04-02
; PRIOR FILING DATE: 2003-04-02
; PRIOR FILING DATE: 2003-04-03
; PRIOR FILING DATE: 2003-04-08
; PRIOR FILING DATE: 2003-04-08
; PRIOR FILING DATE: 2003-04-14
; PRIOR FILING DATE: 2003-04-14
; PRIOR FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2003-04-23
; PRIOR FILING DATE: 2003-04-23
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory syndrome virus
US-10-808-187A-2261

Query Match      73.1%; Score 19; DB 34; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
Db      2 DNFA 5

RESULT 12
US-10-852-357-2255
; Sequence 2255, Application US/10852357
; GENERAL INFORMATION:
; APPLICANT: GUAN, YI
; APPLICANT: ZHENG, BOJIAN
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE PRECURSOR VIRUS OF HUMAN
; FILE REFERENCE: V9661.0081
; CURRENT APPLICATION NUMBER: US/10/852,357
; CURRENT FILING DATE: 2004-05-24
; PRIOR FILING DATE: 2003-05-22
; PRIOR FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 2464
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2255
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory syndrome virus
US-10-852-357-2255

Query Match      73.1%; Score 19; DB 34; Length 5;
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Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
Db      2 DNFA 5

RESULT 13
US-09-855-604-905
; Sequence 905, Application US/09855604
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: COGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 905
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604-905

Query Match      69.2%; Score 18; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNF 4
Db      3 DNF 5

RESULT 14
US-09-855-604A-905
; Sequence 905, Application US/09855604A
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: COGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
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; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 905
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604A-905

Query Match      69.2%; Score 18; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DNF 4
      |||
Db      3 DNF 5

RESULT 15
US-10-111-983-7056
; Sequence 7056, Application US/10111983
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: GALEOTTI Cesira
; APPLICANT: GRANDI Guido
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MORA Mariarosa
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: RAPPUOLI Rino
; APPLICANT: RATTI Giulio
; APPLICANT: SCARLATO Vincenzo
; APPLICANT: SCARSELLI Maria
; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES
; FILE REFERENCE: 2300-1654 (PP01654.003)
; CURRENT APPLICATION NUMBER: US/10/111,983
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US-60/162616
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 37764
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7056
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Neisseria
US-10-111-983-7056

Query Match      65.4%; Score 17; DB 27; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LDNFS 5
      |||
Db      1 LSNFA 5

Search completed: September 10, 2005, 01:24:35
Job time : 481 secs
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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:52:07 ; Search time 41 Seconds
(without alignments)
18.207 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WEYFIAAEV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 16468

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	4	US-09-911-129B-6
2	33	60.0	10	4	US-09-911-129B-5
3	26	47.3	10	3	US-08-159-339A-1219
4	24	43.6	10	1	US-08-433-318A-146
5	24	43.6	10	1	US-08-433-318A-147
6	24	43.6	10	1	US-08-433-318A-148
7	24	43.6	10	1	US-08-433-318A-149
8	24	43.6	10	2	US-08-406-330-3
9	24	43.6	10	2	US-08-556-597-3
10	24	43.6	10	2	US-08-922-048-146
11	24	43.6	10	2	US-08-922-048-147
12	24	43.6	10	2	US-08-922-048-148
13	24	43.6	10	2	US-08-922-048-149
14	24	43.6	10	3	US-08-531-832A-1
15	24	43.6	10	3	US-09-315-304B-1572
16	24	43.6	10	3	US-09-315-304B-1573
17	24	43.6	10	3	US-09-315-304B-1584
18	24	43.6	10	3	US-09-315-304B-1585
19	24	43.6	10	4	US-09-111-681C-162
20	24	43.6	10	4	US-09-111-681C-163
21	24	43.6	10	4	US-09-111-681C-164
22	24	43.6	10	4	US-09-111-681C-165
23	24	43.6	10	4	US-09-350-325-32
24	24	43.6	10	4	US-09-350-325-33
25	24	43.6	10	4	US-09-350-325-44
26	24	43.6	10	4	US-09-350-325-45
27	24	43.6	10	4	US-09-350-641C-1572

28	24	43.6	10	4	US-09-350-641C-1573
29	24	43.6	10	4	US-09-350-641C-1584
30	24	43.6	10	4	US-09-350-641C-1585
31	24	43.6	10	5	PCT-US96-06270-146
32	24	43.6	10	5	PCT-US96-06270-147
33	24	43.6	10	5	PCT-US96-06270-148
34	24	43.6	10	5	PCT-US96-06270-149
35	23	41.8	10	2	US-08-406-330-8
36	23	41.8	10	2	US-08-556-597-8
37	23	41.8	10	3	US-08-822-586-18
38	23	41.8	10	3	US-08-822-586-22
39	23	41.8	10	3	US-08-822-586-26
40	23	41.8	10	3	US-08-371-680-10
41	23	41.8	10	4	US-09-620-091-32
42	23	41.8	10	4	US-09-810-601B-35
43	23	41.8	10	4	US-09-810-601B-37
44	22	40.0	10	4	US-09-755-630B-34
45	22	40.0	10	4	US-09-911-129B-7

ALIGNMENTS

RESULT 1

US-09-911-129B-6
; Sequence 6, Application US/09911129B
; Patent No. 6703364
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalfatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-6

Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	WEYFIAAEV 10
DB	1	WEYFIAAEV 10

RESULT 2

US-09-911-129B-5
; Sequence 5, Application US/09911129B
; Patent No. 6703364
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalfatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-5

Query Match 60.0%; Score 33; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.1; Mismatches 0; Gaps 0; Indels 0;

Qy 1 WEYFI 5
Db 6 WEYFI 10

RESULT 3
US-08-159-339A-1219
; Sequence 1219, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1219

Qy 1 WEYF 4
Db 2 WQYF 5

RESULT 4
US-08-433-318A-146
; Sequence 146, Application US/08433318A
; Patent No. 5663144

Query Match 47.3%; Score 26; DB 3; Length 10;
Best Local Similarity 75.0%; Pred. No. 90;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5663144ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WORDPERFECT 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,318A
; FILING DATE: 03-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-433-318A-146

Query Match 43.6%; Score 24; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
Db 5 WEYF 8

RESULT 5
US-08-433-318A-147
; Sequence 147, Application US/08433318A
; Patent No. 5663144
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5663144ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WORDPERFECT 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,318A

Qy 1 WEYF 4
Db 5 WEYF 8

RESULT 5
US-08-433-318A-147
; Sequence 147, Application US/08433318A
; Patent No. 5663144
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5663144ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WORDPERFECT 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,318A

;; FILING DATE: 03-MAY-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark Deluca
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: UPN-2106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 147:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-433-318A-147

Query Match 43.6%; Score 24; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 5 WEWF 8

RESULT 6
US-08-433-318A-148
;; Sequence 148, Application US/08433318A
;; Patent No. 5663144
;; GENERAL INFORMATION:
;; APPLICANT: Greene, Mark I.
;; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
;; NUMBER OF SEQUENCES: 184
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;; ADDRESSEE: No. 5663144ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: WORDPERFECT 6
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/433,318A
;; FILING DATE: 03-MAY-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark Deluca
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: UPN-2106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 148:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-433-318A-148

Query Match 43.6%; Score 24; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 5 WEWF 8

RESULT 7
US-08-433-318A-149
;; Sequence 149, Application US/08433318A
;; Patent No. 5663144
;; GENERAL INFORMATION:
;; APPLICANT: Greene, Mark I.
;; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
;; NUMBER OF SEQUENCES: 184
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
;; ADDRESSEE: No. 5663144ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: WORDPERFECT 6
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/433,318A
;; FILING DATE: 03-MAY-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark Deluca
;; REGISTRATION NUMBER: 33,229
;; REFERENCE/DOCKET NUMBER: UPN-2106
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 149:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-433-318A-149

Query Match 43.6%; Score 24; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 5 WEWF 8

RESULT 8
US-08-406-330-3
;; Sequence 3, Application US/08406330
;; Patent No. 5817748
;; GENERAL INFORMATION:
;; APPLICANT: Miller, Jonathan L.
;; APPLICANT: Lyle, Vicki A.
;; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
;; NUMBER OF SEQUENCES: 81
;; CORRESPONDENCE ADDRESS:
US-08-433-318A-148

ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-3

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 4 WRYP 7

RESULT 9
US-08-556-597-3
Sequence 3, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101

TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-3

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 4 WRYP 7

RESULT 10
US-08-922-048-146
Sequence 146, Application US/08922048
Patent No. 5919764
GENERAL INFORMATION:
APPLICANT: Greene, Mark I.
TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
TITLE OF INVENTION: METHODS OF USING THE SAME
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5919764rls
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows
SOFTWARE: WORDPERFECT 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/922,048
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,318
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mark DeLuca
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: UPN-2106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 146:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-922-048-146

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 5 WEWF 8

RESULT 11

US-08-922-048-147
; Sequence 147, Application US/08922048
; Patent No. 5919764
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5919764ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WORDPERFECT 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,048
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,318
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 147:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-922-048-147

Query Match

43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4

Db 5 WEWF 8

RESULT 12

US-08-922-048-148
; Sequence 148, Application US/08922048
; Patent No. 5919764
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5919764ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH

; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WORDPERFECT 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,048
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,318
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 148:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-922-048-148

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4

Db 5 WEWF 8

RESULT 13

US-08-922-048-149
; Sequence 149, Application US/08922048
; Patent No. 5919764
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5919764ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: WORDPERFECT 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,048
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/433,318
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Deluca
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-2106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10

; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-922-048-149

Query Match 43.6%; Score 24; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
Db 5 WEWF 8

RESULT 14

US-08-531-832A-1
; Sequence 1, Application US/08531832A

; Patent No. 6001964

; GENERAL INFORMATION:

; APPLICANT: BRUCE D. GAYNOR, BETTY A. DIAMOND,

; APPLICANT: MATTHEW D. SCHARFF AND PHILIPPE VALADON

; TITLE OF INVENTION: PEPTIDES FOR THE TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF SYSTEMIC LUPUS

; TITLE OF INVENTION: ERYTHEMATOSUS

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN

; STREET: 90 PARK AVENUE

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: U.S.A.

; ZIP: 10016

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/531,832A

; FILING DATE: SEPTEMBER 20, 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: CRAIG J. ARNOLD

; REGISTRATION NUMBER: 34,287

; REFERENCE/DOCKET NUMBER: 96700/342

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 697-5995

; TELEFAX: (212) 286-0854 or 286-0082

; TELEX: TWX 710-581-4766

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10

; TYPE: AMINO ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; MOLECULE TYPE:

; DESCRIPTION: PEPTIDE

; HYPOTHETICAL: YES

; ANTI-SENSE: NO

US-08-531-832A-1

Query Match 43.6%; Score 24; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEYFI 5
Db 2 WEYSV 6

RESULT 15

US-09-315-304B-1572

; Sequence 1572, Application US/09315304B

; Patent No. 6348568

; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1572
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1572

Query Match 43.6%; Score 24; DB 3; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
Db 7 WEWF 10

Search completed: September 10, 2005, 00:56:55
Job time : 41 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:41:46 ; Search time 15 Seconds
(without alignments)
64.145 Million cell updates/sec

Title: US-10-795-795-6

Perfect score: 55

Sequence: 1 WEYFIAAEV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 311

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.7	10	1 RHSGG	gonadoliberein - pi
2	18	32.7	10	1 RHSGG	gonadoliberein - sh
3	18	32.7	10	1 RHAQ1	gonadoliberein I -
4	18	32.7	10	2 A2114	gonadoliberein - ch
5	17	30.9	10	2 A40753	aldehyde ferredoxi
6	16	29.1	10	2 B33995	hypotrehalosemic h
7	16	29.1	10	2 S59625	beta-galactosidase
8	16	29.1	10	2 S63696	DNA polymerase - y
9	16	29.1	10	2 E49033	T-cell receptor ga
10	16	29.1	10	2 F49033	T-cell receptor ga
11	15	27.3	10	2 S39392	calpain (EC 3.4.22
12	15	27.3	10	2 PT0215	T-cell receptor be
13	15	27.3	10	2 S68033	cytochrome P450 1A
14	14	25.5	10	1 SPRGNK	neurokinin K - pig
15	13	23.6	10	1 A61126	gonadoliberein - sp
16	13	23.6	10	1 RHAQ2	gonadoliberein II -
17	13	23.6	10	2 S71868	glutathione transf
18	13	23.6	10	2 B46030	gonadoliberein II -
19	13	23.6	10	2 C39191	hypothetical prote
20	13	23.6	10	2 PQ0753	beta-fructofuranos
21	13	23.6	10	2 A49187	gonadotropin-relea
22	13	23.6	10	2 S23370	T-cell receptor al
23	13	23.6	10	2 PH0916	T-cell receptor be
24	13	23.6	10	2 S38304	lectin GNL1 alpha
25	13	23.6	10	2 S66248	processing enzyme,
26	13	23.6	10	2 B61440	polysaccharonase
27	13	23.6	10	2 PN0165	triose-phosphate i
28	13	23.6	10	2 B46030	gonadoliberein I -
29	13	23.6	10	2 A44871	monodehydroascorba

gastric juice pept
gonadoliberein - se
6-phosphofructo-2-
pepsin (EC 3.4.23.
caerulein - frog (
caerulein-like pep
PVI protein - huma
triose-phosphate i
alpha-amylase (EC
polygalacturonase
polygalacturonase
clotting protein -
serum heterodimer,
bradykinin-potent
NADH2 dehydrogenas
angiotensin-conver

ALIGNMENTS

RESULT 1

RHPGG

gonadoliberein - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997

C:Accession: A01411

R:Baba, Y.; Matsuo, H.; Schally, A.V.

Biochem. Biophys. Res. Commun. 44, 459-463, 1971

A:Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of th.

A:Reference number: A90172; MUID:72114303; PMID:4946067

A:Accession: A01411

A:Molecule type: protein

A:Residues: 1-10 <BAB>

R:Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.

Biochem. Biophys. Res. Commun. 45, 822-827, 1971

A:Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase meth.

A:Reference number: A90176; MUID:72065376; PMID:4942726

A:Contents: annotation; synthesis

A:Note: the synthetic and natural hormones have the same physicochemical and biological

R:Baba, Y.; Arimura, A.; Schally, A.V.

Biochem. Biophys. Res. Commun. 45, 483-487, 1971

A:Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.

A:Reference number: A90175; MUID:72117544; PMID:4946275

A:Contents: annotation

A:Note: Trp-3 appears to be essential for biological activity

C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and f.

C:Superfamily: gonadoliberein

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.7%; Score 18; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.2e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

Db 3 WSY 5

RESULT 2

RHSHG

gonadoliberein - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997

C:Accession: A93780; A01411

R:Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, R.; B

Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972

A:Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing fact

A:Reference number: A93780; MUID:72094314; PMID:4550508

A:Accession: A93780

A:Molecule type: protein

A;Residues: 1-10 <BUR>
 A;Note: the natural and synthetic hormones have the same biological activity
 C;Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and follicle stimulating hormone
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.7%; Score 18; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.2e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

DB 3 WSY 5

RESULT 3

RHAQ1

Gonadoliberin I - American alligator

N;Alternate names: gonadotropin-releasing hormone I

C;Species: Alligator mississippiensis (American alligator)

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C;Accession: A60066

R;Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
 Regul. Pept. 33, 105-116, 1991

A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of
 A;Reference number: A60066; MUID:91352338; PMID:1882082

A;Accession: A60066

A;Molecule type: protein

A;Residues: 1-10 <LOW>

C;Cross-references: UNIPROT:P37041

C;Superfamily: gonadoliberin

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.7%; Score 18; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.2e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

DB 3 WSY 5

RESULT 4

A21114

Gonadoliberin - chum salmon

C;Species: Oncorhynchus keta (chum salmon)

C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 09-Jul-2004

C;Accession: A21114

R;Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W.

Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983

A;Title: Characterization of a teleost gonadotropin-releasing hormone.

A;Reference number: A21114; MUID:83195140; PMID:6341999

A;Accession: A21114

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <SHE>

A;Cross-references: UNIPROT:P20367

Query Match

Best Local Similarity 32.7%; Score 18; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

DB 3 WSY 5

RESULT 5

A40753

aldehyde ferredoxin oxidoreductase (EC 1.2.7.-) - Pyrococcus furiosus (fragment)
 N;Alternate names: glyceraldehyde:ferredoxin oxidoreductase; red tungsten protein (RTP)
 C;Species: Pyrococcus furiosus
 C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 09-Jul-2004

C;Accession: A40753

R;Mukund, S.; Adams, M.W.W.

J. Biol. Chem. 266, 14208-14216, 1991

A;Title: The novel tungsten-iron-sulfur protein of the hyperthermophilic archaeobacterium
 colytic pathway.

A;Reference number: A40753; MUID:91317766; PMID:1907273

A;Accession: A40753

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <MUK>

A;Cross-references: UNIPROT:Q7M530

C;Keywords: iron-sulfur protein; oxidoreductase; tungsten

Query Match 30.9%; Score 17; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 3.4e+03;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WEYFI 5

DB 5 WGRFI 9

RESULT 6

B33995

hypotrehalosemic hormone - black horse fly

C;Species: Tabanus atratus (black horse fly)

C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-Jul-2004

C;Accession: B33995

R;Jaffe, H.; Ratna, A.K.; Riley, C.T.; Fraser, B.A.; Nachman, R.J.; Vogel, V.W.; Zhang,

Proc. Natl. Acad. Sci. U.S.A. 86, 8161-8164, 1989

A;Title: Primary structure of two neuro peptide hormones with adipokinetic and hypotrehal

A;Reference number: A33995; MUID:90046758; PMID:2813385

A;Accession: B33995

A;Molecule type: protein

A;Residues: 1-10 <JAP>

A;Cross-references: UNIPROT:P14596

C;Superfamily: adipokinetic hormone

C;Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F;10/Modified site: amidated carboxyl end (Tyr) #status predicted

Query Match

Best Local Similarity 29.1%; Score 16; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

DB 8 WGY 10

RESULT 7

S59625

beta-galactosidase alpha chain - Escherichia coli (fragment)

C;Species: Escherichia coli

C;Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C;Accession: S59625

R;Calugaru, S.V.; Hall, B.G.; Sinnott, M.L.

Biochem. J. 312, 281-286, 1995

A;Title: Catalysis by the large subunit of the second beta-galactosidase of Escherichia

A;Reference number: S59625; MUID:96077156; PMID:7492325

A;Accession: S59625

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <CAL>

Query Match

Best Local Similarity 29.1%; Score 16; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WE 2
||
Db 4 WE 5

RESULT 8

DNA polymerase - yeast (*Kluyveromyces marxianus* var. *lactis*) killer plasmid pGKL2 (fragment)
A:Species: *Kluyveromyces marxianus* var. *lactis*, *Candida sphaerica*
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 25-Apr-1997
C:Accession: S63696
R:Takeda, M.; Hiraishi, H.; Takesako, T.; Tanase, S.; Gunge, N.
Yeast 12, 241-246, 1996
A:Title: The terminal protein of the linear DNA plasmid pGKL2 shares an N-terminal domain with the terminal protein of the linear DNA plasmid pGKL2
A:Reference number: S63696; MUID:97060015; PMID:8904336
A:Accession: S63696
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <TAK>
A>Note: the source is designated as *Kluyveromyces lactis*

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WE 2
||
Db 4 WE 5

RESULT 9

E49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 19-Dec-1993 #sequence_revision 25-Aug-1995 #text_change 21-Jul-2000
C:Accession: E49033; D49033
R:Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A:Title: Functionally distinct subsets of human gamma/delta T cells.
A:Reference number: A49033; MUID:92083926; PMID:1684157

A:Accession: E49033
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <MOR>
A:Cross-references: GB:S72587; NID:G240696; PIDN:AAB20630.1; PID:G240697
A>Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIIP:72595)
A:Accession: D49033
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <MOR>
A:Cross-references: GB:S72587; NID:G240696; PIDN:AAB20630.1; PID:G240697
A>Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIIP:72589)
C:Keywords: T-cell receptor

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WE 2
||
Db 4 WE 5

RESULT 10

F49033
T-cell receptor gamma chain V-D-J region - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 19-Dec-1993 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: F49033
R:Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.
Eur. J. Immunol. 21, 2999-3007, 1991
A:Title: Functionally distinct subsets of human gamma/delta T cells.
A:Reference number: A49033; MUID:92083926; PMID:1684157

A:Accession: F49033
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <MOR>
A:Cross-references: GB:S72605; NID:G240700; PIDN:AAB20632.1; PID:G240701
A>Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIIP:72606)
C:Keywords: T-cell receptor

Query Match 29.1%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WE 2
||
Db 4 WE 5

RESULT 11

S39392
calpain (BC 3.4.22.17) II light chain - pig (fragment)
C:Species: *Sus scrofa domestica* (domestic pig)
C:Date: 18-Feb-1994 #sequence_revision 24-Jul-1998 #text_change 29-Sep-1999
C:Accession: S39392
R:Crawford, C.; Brown, N.R.; Willis, A.C.
Biochem. J. 296, 135-142, 1993
A:Title: Studies of the active site of m-calpain and the interaction with calpastatin.
A:Reference number: S39391; MUID:94071815; PMID:8250833

A:Accession: S39392
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <CRA>
C:Superfamily: calpain small chain; calmodulin repeat homology
C:Keywords: cysteine proteinase; EF hand; hydrolase

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ABEV 10
|||
Db 4 SEEV 7

RESULT 12

PT0215
T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0215
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted by the T cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)
A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0215
A:Molecule type: mRNA
A:Residues: 1-10 <NAK>
C:Keywords: T-cell receptor

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.4e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EYF 4
||
Db 8 QYF 10

RESULT 13

S68033
cytochrome P450 1A1 - tilapia (fragment)
C:Species: *Oreochromis niloticus* x *Oreochromis aureus* (tilapia)
C:Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C:Accession: S68033

R;Ueng, Y.F.; Ueng, T.H.
 Arch. Biochem. Biophys. 322, 347-356, 1995
 A;Title: Induction and purification of cytochrome P450 1A1 from 3-methylcholanthrene-treated rats
 A;Reference number: S68033; MUID:96032654; PMID:7574707
 A;Accession: S68033
 A;Molecule type: protein
 A;Residues: 1-10 <UEN>
 A;Experimental source: liver and gill

Db 3 WSH 5

Search completed: September 10, 2005, 00:56:08
 Job time : 16 secs

Query Match 27.3%; Score 15; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 8.4e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 FIAAEV 10
 ||||
 DB 4 FIGALSV 10

RESULT 14
 SPFGNK
 neuromedin K - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
 C;Accession: A01560
 R;Kangawa K.; Minamino, N.; Fukuda, A.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 114, 533-540, 1983
 A;Title: Neuromedin K: a novel mammalian tachykinin identified in porcine spinal cord.
 A;Reference number: A01560; MUID:83282812; PMID:6576785
 A;Accession: A01560
 A;Molecule type: protein
 A;Residues: 1-10 <KAN>
 A;Cross-references: UNIPROT:P01292
 A;Note: the structure of the peptide was confirmed by synthesis
 C;Comment: The biological source of this peptide is spinal cord. It stimulates smooth muscle contraction.
 C;Superfamily: neurokinin B precursor
 C;Keywords: amidated carboxyl end; hormone; spinal cord
 P;10/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 25.5%; Score 14; DB 1; Length 10;
 Best Local Similarity 25.0%; Pred. No. 1.3e+04;
 Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYFI 5
 :||:
 DB 4 DFFV 7

RESULT 15
 A61126
 gonadoliberin - spotted ratfish
 N;Alternate names: gonadotropin-releasing hormone
 C;Species: Hydrolagus colliei (spotted ratfish)
 C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
 C;Accession: A61126
 R;Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.
 Gen. Comp. Endocrinol. 82, 152-161, 1991
 A;Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocarpine fish.
 A;Reference number: A61126; MUID:91340067; PMID:1678723
 A;Accession: A61126
 A;Molecule type: protein
 A;Residues: 1-10 <LOV>
 A;Cross-references: UNIPROT:P37043
 A;Experimental source: brain
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid
 P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 P;10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.6%; Score 13; DB 1; Length 10;
 Best Local Similarity 33.3%; Pred. No. 2.1e+04;
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:56:13 ; Search time 162 Seconds
(without alignments)
11.937 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LONFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 26026

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	5	6	ABU62026
2	26	100.0	5	8	ADS64548
3	19	73.1	5	8	ADM09689
4	19	73.1	5	8	ADR70855
5	17	65.4	5	6	ABU12290
6	16	61.5	5	1	AAP83010
7	16	61.5	5	1	AAP91831
8	16	61.5	5	2	AAR26902
9	16	61.5	5	2	AAR28940
10	16	61.5	5	2	AAR44338
11	16	61.5	5	2	AAR59489
12	16	61.5	5	2	AAR61484
13	16	61.5	5	2	AAR75581
14	16	61.5	5	2	AAR75592
15	16	61.5	5	2	AAR97812
16	16	61.5	5	2	AAR98996
17	16	61.5	5	2	AAR80273
18	16	61.5	5	2	AAR54223
19	16	61.5	5	2	AAR83536
20	16	61.5	5	3	AAY61720
21	16	61.5	5	3	AAY61887
22	16	61.5	5	4	AAB99511
23	16	61.5	5	5	ABP51750
24	16	61.5	5	5	ABU12288
25	16	61.5	5	6	ABU12289

ALIGNMENTS

RESULT 1

ABU62026

ID ABU62026 standard; peptide; 5 AA.

XX AC ABU62026;

XX DT 26-AUG-2003 (first entry)

XX DE Human blood coagulation factor Va peptide, L5S.

XX KW Human; blood coagulation factor Va; blood clotting factor Va;

KW prothrombinase inhibition; prothrombinase-inhibiting peptide;

KW blood clotting disorder; thrombotic disorder; blood clot formation;

KW blood vessel obstruction; coronary artery disease; unstable angina;

KW valvular heart disease; stable angina; myocardial infarction;

XX KW atrial fibrillation; stroke; blood anticoagulation; anticoagulant.

XX OS Homo sapiens.

XX US2003040600-A1.

XX PD 27-FEB-2003.

XX PF 23-JUL-2001; 2001US-00911129.

XX PR 23-JUL-2001; 2001US-00911129.

XX PA (KALA/) KALAFATIS M.

XX PA (MANN/) MANN K.

XX PI Kalafatis M, Mann K;

XX DR WPI; 2003-492177/46.

XX PT Novel anticoagulant peptide derived from the amino acid region 307-356 of

PT human blood clotting factor Va, useful for preventing thrombotic

PT disorders resulting from formation of blood clots that obstruct blood

PS vessels.

PS Claim 10; Fig 2; 20pp; English.

XX CC The present invention relates to peptides derived from human blood

CC coagulation (clotting) factor Va which exhibit inhibition of

CC the prothrombinase. A pharmaceutical composition comprising one or more of

CC the prothrombinase-inhibiting peptides may be used for treating human

CC subjects with blood clotting disorders. The peptides are useful for

CC preventing thrombotic disorders resulting from the formation of blood

CC clots that obstruct blood vessels, e.g. due to a condition chosen from

ABR62039 CTL activ
AAW41379 CDR1 of h
AAY62384 Cadherin-
AAY62468 Cadherin-
ABR61866 Mouse MAB
Adj81521 Plant ret
Adq31247 CDR1 pept
AdS82646 Anti-IL-2
Aap93096 Region of
AAW41862 Peptide u
AAW59036 Bovine gr
AAW58736 Allergen
AAW92313 E2A/pbx1
AAY79279 G alpha p
AAY62383 Cadherin-
AAB57328 Tn7 trans
ABG93520 Human P-g
ABG62756 Eubacteri
ABG62760 Eubacteri
ABB05808 Amb a I a

CC coronary artery disease, valvular heart disease, stable and unstable
 CC angina, myocardial infarction, atrial fibrillation and stroke. The
 CC peptides of the invention exhibit an IC50 of between 50 nM-500 microm
 CC for inhibition of prothrombinase. The peptides exhibit excellent blood
 CC anticoagulation properties with little or no adverse side effects. The
 CC present sequence represents a peptide that inhibits prothrombinase
 CC activity

XX
 XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 6; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
 |||||
 Db 1 LDNFS 5

RESULT 2

ADS64548
 ID ADS64548 standard; peptide; 5 AA.

XX
 AC ADS64548;

XX
 DT 16-DEC-2004 (first entry)

XX
 DE Human blood coagulation factor Va peptide, L5S.

XX
 KW Prothrombinase inhibitor; human; blood coagulation factor Va;
 KW blood clotting disorder; thrombotic disorder; thrombolytic.

XX
 OS Homo sapiens.

XX
 PN US2004186271-A1.

XX
 PD 23-SEP-2004.

XX
 PF 08-MAR-2004; 2004US-00795795.

XX
 PR 23-JUL-2001; 2001US-00911129.

XX
 PA (KALA/) KALAPATIS M.

XX
 PA (MANN/) MANN K G.

XX
 PI Kalafatis M, Mann KG;

XX
 PD WPI; 2004-689241/67.

XX
 PS New prothrombinase-inhibiting peptide derived from a specific amino acid
 PT sequence of human blood coagulation factor Va, useful for treating human
 PT subjects with blood clotting disorders.

XX
 PS Claim 10; SEQ ID NO 12; 20pp; English.

XX
 CC The present invention relates to a prothrombinase-inhibiting peptide
 CC derived from a specific amino acid sequence of human blood coagulation
 CC factor Va. The invention is useful for treating human subjects with blood
 CC clotting disorders. The invention is also useful for preventing
 CC thrombotic disorders resulting from formation of blood clots that
 CC obstructs blood vessels. The present sequence is the human blood
 CC coagulation factor Va peptide.

XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 8; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
 |||||
 Db 1 LDNFS 5

RESULT 3

ADM09689
 ID ADM09689 standard; peptide; 5 AA.

XX
 AC ADM09689;

XX
 DT 20-MAY-2004 (first entry)

XX
 DE Human proteome unique recognition sequence (URS) seqid 13.

XX
 KW soluble peptide analyte; unique recognition sequence; URS;
 KW protein detection; clinical diagnosis; environmental diagnosis;
 KW drug discovery; protein sequencing; pathogen detection; toxin detection;
 KW anthrax toxin; small pox toxin; cholera toxin;
 KW packaged protein detection array; protein expression profile;
 KW drug screening; protein characterisation; disease prognosis;
 KW pathologic cell profiling; proteome epitope tag; human; proteome.

XX
 OS Homo sapiens.

XX
 PN US2004038307-A1.

XX
 PD 26-FEB-2004.

XX
 PF 12-MAY-2003; 2003US-00436549.

XX
 PR 10-MAY-2002; 2002US-0379626P.

XX
 PR 01-JUL-2002; 2002US-0393137P.

XX
 PR 01-JUL-2002; 2002US-0393197P.

XX
 PR 01-JUL-2002; 2002US-0393211P.

XX
 PR 01-JUL-2002; 2002US-0393223P.

XX
 PR 01-JUL-2002; 2002US-0393233P.

XX
 PR 01-JUL-2002; 2002US-0393280P.

XX
 PR 04-DEC-2002; 2002US-0430948P.

XX
 PR 13-DEC-2002; 2002US-0433319P.

XX
 PA (ENGE-) ENGNEOS INC.

XX
 PI Lee FD, Meng X, Chan JW, Zhang S, Benkovic SJ;

XX
 PD WPI; 2004-327083/30.

XX
 PT Detecting proteins comprises providing solution of soluble peptide
 PT analytes, contacting solution with capture agents capable of interacting
 PT with unique recognition sequence of protein and detecting binding between
 PT agents and analytes.

XX
 PS Claim 60; SEQ ID NO 13; 134pp; English.

XX
 CC The invention describes a method of detecting proteins in sample. The
 CC method comprises: providing a solution of soluble peptide analytes
 CC produced by denaturation and/or cleavage of several sample proteins, and
 CC optionally, labeling the collection of peptides by a detectable part;
 CC contacting the solution with one or more capture agent(s), where each of
 CC the capture agent(s) is able to specifically recognise and interact with
 CC a unique recognition sequence (URS) of a reference protein; and detecting
 CC the binding between one or more of the capture agent(s) and the peptide
 CC analytes, where the detection of binding between a capture agent and a
 CC peptide analyte indicates the presence of the reference protein in the
 CC several of sample proteins. Also described are; a method of
 CC quantifying proteins in a biological sample; a method of simultaneously
 CC detecting several specific proteins in a multi-protein sample. The method
 CC of the invention is used in clinical or environmental diagnosis, drug
 CC discovery, protein sequencing and for the detection of a pathogen or
 CC toxins (such as anthrax toxin, small pox toxin, and cholera toxin). A
 CC packaged protein detection array is useful for: quantifying various forms
 CC of post-translationally modified proteins in a biological sample;
 CC screening large libraries of natural or synthetic compounds to identify
 CC competitors of natural or non-natural ligands for the capture agent,
 CC which may be of diagnostic, prognostic, therapeutic or scientific
 CC interest; and to study the relationship between a subject protein

CC expression profile and that subjects response to a foreign compound or
 CC drug. The methods of assaying differential protein expression are useful
 CC in the identification and validation of new potential drug targets as
 CC well as for drug screening. The capture agents are useful for protein
 CC characterisation, for screening, making prognosis of disease outcomes and
 CC providing treatment modality suggestion based on the profiling of the
 CC pathologic cells, prognosis of the outcome of a normal lesion and
 CC susceptibility of lesions to malignant transformation. The methods
 CC described are useful for identifying and/or detecting a specific organism
 CC based on the organisms proteome epitope tag. This is the amino acid
 CC sequence of a human proteome unique recognition sequence (URS).

XX Sequence 5 AA;

Query Match 73.1%; Score 19; DB 8; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
 |||:
 Db 1 DNFN 4

RESULT 4

ADR70855
 ID ADR70855 standard; peptide; 5 AA.

XX AC ADR70855;

DT 02-DEC-2004 (first entry)

DE Human proteome epitope tag (PET) ENSP00000000412 #4.

XX Human; Protein Epitope Tag; PET: post-translational modification;

KW epitope; kinase; proteome; severe acquired respiratory syndrome; SARS.

XX Homo sapiens.

XX US2004180380-A1.

XX 16-SEP-2004.

PF 13-NOV-2003; 2003US-00712425.

XX 10-MAY-2002; 2002US-0379626P.

PR 01-JUL-2002; 2002US-0393137P.

PR 01-JUL-2002; 2002US-0393197P.

PR 01-JUL-2002; 2002US-0393211P.

PR 01-JUL-2002; 2002US-0393223P.

PR 01-JUL-2002; 2002US-0393233P.

PR 01-JUL-2002; 2002US-0393235P.

PR 01-JUL-2002; 2002US-0393280P.

PR 04-DEC-2002; 2002US-0430948P.

PR 13-DEC-2002; 2002US-0433319P.

PR 12-MAY-2003; 2003US-00436549.

XX (ENGB-) ENGINEOS INC.

PI Lee FD, Meng X, Livingston D;

XX WPI; 2004-675602/66.

XX Detecting post-translational modification on target protein in sample, by
 PT generating capture agent using target fragment sequence with modification
 PT site and epitope tag, contacting sample with agent, detecting fragment
 PT bound to agent.

XX Example 3; SEQ ID NO 13; 309pp; English.

XX The invention relates to detecting the presence of a post-translational

CC modification on a target protein within a sample involving

CC computationally analysing the amino acid sequence of the target protein

CC to identify one or more candidate site for the post-translational

CC modification, computationally identifying the amino acid sequence of one
 CC or more fragment of the target protein (where the fragment predictably
 CC results from a treatment of the target protein within the sample, and the
 CC fragment encompasses the potential post-translational modification site
 CC and a protein epitope tag (PET) unique to the fragment within the
 CC sample), generating a capture agent that specifically binds the PET,
 CC immobilising the capture agent to a support, subjecting the sample to the
 CC treatment to render the fragment soluble in solution, contacting the
 CC sample after the treatment to the capture agent and detecting in the
 CC fragment bound to the capture agent the presence or absence of the post-
 CC translational modification. Also included an array of capture agent for
 CC identifying all potential substrates of a kinase (or enzyme catalyzing
 CC post-translational modification) within a proteome, identifying (M2), in
 CC a sample, a potential substrates of a kinase (or potential substrates of
 CC an enzyme that catalyses a post-translational modification chosen from
 CC acetylation, amidation, deamidation, prenylation, formylation,
 CC glycosylation, hydroxylation, methylation, myristoylation, an array
 CC of capture agents for determining which of a selected number of signal
 CC transduction pathways within a proteome is activated or inhibited in
 CC response to a stimulation, a business method for a biotechnology or
 CC pharmaceutical business (involving identifying one or more substrates for
 CC an enzyme catalysing a post-translational modification using (M2),
 CC optionally, verifying the post-translational modification of the
 CC substrates by the enzyme, and licensing to a third party the right to
 CC manufacture, or explore the use of the substrate as a target of the
 CC enzyme), a composition (C1) comprising several capture agents (where the
 CC several capture agents are collectively capable of specifically
 CC interacting with all potential substrates of a post-translational
 CC modification enzyme within an organisms proteome, and each of the capture
 CC agents is able to recognised and interact with only one PET within the
 CC potential substrate or its fragment containing the post-translational
 CC modification site), immunising a host animal against a disease condition
 CC associated with the presence or overexpression of a protein, generating
 CC antibodies specific for a marker protein for use in immunohistochemistry
 CC (involving computationally analysing the amino acid sequence of the
 CC marker protein to identify one or more PET(s) unique to the marker
 CC protein, where the PET(s) is located on the surface of marker protein), a
 CC method for simultaneous unambiguous detection quantification of a family
 CC of related proteins in a sample, processing a sample for use in PET-
 CC associated detection/quantitation of a target protein in the sample, a
 CC severe acquired respiratory syndrome (SARS) virus-specific PET amino acid
 CC sequence as given in the specification and generating antibodies specific
 CC for a PET sequence. The method is useful for detecting the presence of
 CC post-translational modification on a target protein within a sample
 CC obtained from human, mouse, rat, frog (Xenopus), fish (zebra fish), fly
 CC (Drosophila melanogaster), nematode (C. elegans), fission or budding
 CC yeast or plant (Arabidopsis thaliana). The method is useful for
 CC identifying a potential substrates of kinase or enzyme that catalyze a
 CC post-translational modification. The array is useful for identifying all
 CC potential substrates of a kinase or enzyme catalysing post-translational
 CC modification within a proteome or for determining which of a selected
 CC number of signal transduction pathways within a sample from a proteome is
 CC activated or inhibited in response to a stimulation. The present sequence
 CC is a PET peptide of the invention.

XX Sequence 5 AA;

Query Match 73.1%; Score 19; DB 8; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
 |||:
 Db 1 DNFN 4

RESULT 5

ABU12290

ID ABU12290 standard; peptide; 5 AA.

XX ABU12290;

XX

DT 18-FEB-2003 (first entry)
 XX Chymotrypsin inhibitor 2, 3C12, alpha helix prediction pentapeptide #54.
 DE
 XX
 KW ASTRO-FOLD; ab initio; alpha-helix; beta-sheet; disulphide bridge;
 KW atomistic modelling; low energy conformation; entropic energy;
 KW free energy; equilibrium probability; helical cluster; integer-linear;
 KW mathematical model; hydrophobic contact energy;
 KW atom force field potential; global optimisation; torsion angle;
 KW dynamic algorithm; three-dimensional structure; tertiary structure;
 KW chymotrypsin inhibitor; 3C12.
 XX
 OS Hordeum vulgare.
 XX
 XX WO200279872-A2.
 XX
 XX 10-OCT-2002.
 XX
 XX 19-FEB-2002; 2002WO-US004644.
 XX
 XX 16-FEB-2001; 2001US-00788006.
 XX (UVP-1) UNIV PRINCETON.
 XX
 XX Floudas CA, Klepeis JL;
 PI
 XX WPI; 2003-059449/05.
 DR
 XX
 XX Determining helix regions, and beta sheets of polypeptide, involves
 PT partitioning peptide, atomistic modeling by selected force, generating
 PT ensemble low energy, and calculating free energies for each peptide.
 XX
 XX Example 1; Page 62; 147pp; English.
 PS
 XX
 XX The invention discloses a ASTRO-FOLD approach for the ab initio
 CC prediction method for determining the existence and location of alpha-
 CC helix regions and arrangement of beta-sheets and disulphide bridges of a
 CC polypeptide. The method comprises defining the first segment of the amino
 CC acid sequence, performing atomistic modelling upon each segment,
 CC generating an ensemble of low energy conformations, determining the
 CC entropic and free energy for each segment and then ascertaining the
 CC equilibrium probabilities for helical clusters. The segments consist of
 CC pentapeptides, with each further segment including a majority of the
 CC amino acid residues of the first segment, together with an additional
 CC amino acid residue(s), adjacent to the first amino acid sequence. The
 CC beta-sheets and disulphide bridges of a polypeptide are determined by
 CC identifying a superstructure encompassing alternative beta-strand
 CC arrangements, representing the superstructure by an integer-linear
 CC programming mathematical model, with the model maximising the total
 CC hydrophobic contact energy, and then solving the model. The method can
 CC also apply energy modelling with a full atom force field potential to
 CC generate a constrained global optimisation problem, optionally applying a
 CC torsion angle dynamics algorithm and then solving the constrained global
 CC optimisation problem to determine the three-dimensional structure of the
 CC polypeptide. The method is useful for determining the tertiary structure
 CC of a polypeptide and is accurate and reliable. The sequences presented in
 CC ABU1237-ABU12295 are the pentapeptides of the chymotrypsin inhibitor,
 CC 3C12, which were used to predict the alpha-helical regions in an example
 CC of the method of the invention
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 65.4%; Score 17; DB 6; Length 5;
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 LDNFS 5
 Db ||| :
 1 LDNIA 5
 RESULT 6
 AAP83010

ID AAP83010 standard; protein; 5 AA.
 XX
 AC AAP83010;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-DEC-1990 (first entry)
 XX
 XX Blocking peptide used in composition for treatment and diagnosis of HIV
 DE infections.
 XX
 KW HIV; gp110; monoclonal antibodies; neutralising region.
 XX
 OS Homo sapiens.
 XX
 XX GB2196634-A.
 XX
 XX 05-MAY-1988.
 XX
 XX 19-AUG-1987; 87GB-00019587.
 XX
 XX 20-AUG-1986; 86US-00898273.
 PR 01-MAY-1987; 87US-00045026.
 PR 29-JUN-1987; 87US-00067996.
 PR 07-OCT-1987; 87US-00105761.
 XX
 XX (GENE-) GENETIC SYSTEMS CORP.
 PA
 XX Shriver MK;
 XX
 XX WPI; 1988-103268/15.
 DR
 XX Monoclonal antibodies and peptide(s) - useful for treatment and diagnosis
 PT of human immuno-deficiency virus infections.
 XX
 XX Claim 42; Page 24; 25pp; English.
 PS
 XX This is a blocking peptide which inhibits virus proliferation. It is
 CC useful, in conjunction with a monoclonal antibody to a neutralising
 CC region of HIV, for treatment or prophylaxis of HIV infections. N- and C-
 CC terminals can have up to 20 amino acids attached. See also AAP83003-09
 CC and AAP83011-12. This is equivalent to N8701950 (accession no. 1s from
 CC this). (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-
 CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct DR field.)
 XX
 XX Sequence 5 AA;
 SQ
 Query Match 61.5%; Score 16; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DNFS 5
 Db ||| :
 2 DNYT 5
 RESULT 7
 AAP91831
 ID AAP91831 standard; protein; 5 AA.
 XX
 AC AAP91831;
 XX
 XX 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 22-MAY-1990 (first entry)
 XX
 XX Pentapeptide which inhibits HIV binding to cell surface receptors.
 DE HIV; psoriasis; neuropsychiatric disorders.
 XX
 XX Unidentified.
 OS
 XX USN7352313-N.
 PN

XX PD 10-OCT-1989.
 XX PF 16-MAY-1989; 89US-00352313.
 XX PR 27-MAY-1988; 88US-00199873.
 XX PR 18-DEC-1988; 88US-00285559.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX PA (USDC) US SEC OF COMMERCE.
 XX PI Bridge P, Goodwin FK;
 XX DR WPI; 1989-378088/51.
 XX PT Use of short peptide(s) to inhibit binding of HIV to human cells - for
 XX PT treating psoriasis and neuro-psychiatric disorder including memory
 XX PT deficiency and mood disorder.
 XX PS Disclosure; Page 8; 18pp; English.
 XX CC This peptide is used in a composition for treatment of chronic conditions
 XX CC eg neuropsychiatric disorders and psoriasis through inhibition of HIV-
 XX CC cell surface receptor (CD4) binding. CD4 site is common to the CNS and
 XX CC immune system. AIDS- and non AIDS-related psoriasis both respond
 XX CC favourably to treatment with the peptide-containing composition. There
 XX CC are a range of forms which the composition and administration can take.
 XX CC The aspartic acid residue can be replaced by a threonine residue.
 XX CC Analogues with D-threonine at the amino-terminal and/or an amide deriv-
 XX CC ative at the carboxy-terminal can be used. (Note: Revised entry submitted
 XX CC to correct the patent number format of US Government-owned NTIS
 XX CC applications to prevent clashes with ongoing US granted patent numbers.
 XX CC For further information please visit the Derwent web site at
 XX CC www.derwent.com/dwpi/updates/ntis us.html) (Updated on 10-MAR-2003 to
 XX CC add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.)
 XX CC (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 5 AA;

Query Match 61.5%; Score 16; DB 1; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNFS 5
 Db ||:::
 2 DNYT 5

RESULT 8
 AAR26902
 ID AAR26902 standard; peptide; 5 AA.
 XX AC AAR26902;
 XX DT 25-MAR-2003 (revised)
 XX DT 20-MAY-1998 (first entry)
 XX DE Herpes simplex virus treatment peptide.
 XX XX HSV; HSV-1; HSV-2; Varicella Zoster virus; human cytomegalovirus;
 KW Epstein-Barr virus.
 XX OS Synthetic.
 XX PN WO9214751-A1.
 XX PD 03-SEP-1992.
 XX PF 24-FEB-1992; 92WO-DK000053.
 XX PR 25-FEB-1991; 91DK-00000319.
 XX PA (CARL-) CARLBIOTECH LTD AS.

XX PI Pedersen O, Macfadden DK;
 XX DR WPI; 1992-316120/38.
 XX PT New linear or cyclic peptide(s) including cysteine residue - occupy
 XX PT lymphocyte CD4 receptors, for treating and preventing virus infections
 XX PT with Herpes simplex, Varicella zoster, cytomegalovirus and Epstein-Barr
 XX PT virus.
 XX PS Claim 5; Page 15; 21pp; English.
 XX CC The peptide is useful in the treatment and prevention of diseases or
 XX CC conditions caused by Herpes viruses, esp. Herpes Simplex Virus-1 (HSV-1),
 XX CC HSV-2, Varicella Zoster Virus (VZV), human cytomegalovirus (HCV) or
 XX CC Epstein-Barr Virus (EBV). It can also be used to treat diseases and
 XX CC conditions caused by the family of herpes viruses in animals, e.g.
 XX CC Aujeszky's disease in pigs, bovine rhinotracheitis, rhinopharyngitis in
 XX CC horses, laryngotracheitis in poultry and Marek's disease in chickens. It
 XX CC can also be used in diagnostics. The peptide has never been reported to
 XX CC penetrate any type of cells, but only to occupy the CD4 receptors found
 XX CC on lymphocytes and it apparently penetrates the skin with relative ease.
 XX CC A major advantage of the peptide is its almost complete lack of toxicity,
 XX CC which means that the use of high doses for an extended period of time is
 XX CC possible without use of high doses for an extended period of time is
 XX CC possible without any drawbacks. It is an example of a highly generic
 XX CC peptide (AAR26905,6). See also AAR26901-R26906. (Updated on 25-MAR-2003
 XX CC to correct PN field.) (Updated on 25-MAR-2003 to correct PF field.)
 XX SQ Sequence 5 AA;
 Query Match 61.5%; Score 16; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNFS 5
 Db ||:::
 2 DNYT 5

RESULT 9
 AAR28940
 ID AAR28940 standard; peptide; 5 AA.
 XX AC AAR28940;
 XX DT 25-MAR-2003 (revised)
 XX DT 23-MAR-1993 (first entry)
 XX DE Example of a generic peptide for treating chronic fatigue syndrome.
 XX XX CFS; fatigue; tension; anger; confusion; peptide T; HIV; synthetic;
 KW human immunodeficiency virus; gp 120.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 1 /note= "Thr or D-Thr"
 XX FT Modified-site 5 /note= "may be amidated"
 XX FT
 XX PN WO9219257-A1.
 XX PD 12-NOV-1992.
 XX PF 08-MAY-1992; 92WO-US003582.
 XX PR 08-MAY-1991; 91US-00696556.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX PI Bridge TP, Goodwin FK;

XX WPI; 1992-398525/48.
 XX
 PT Peptide compens. for treating chronic fatigue syndrome - ameliorate
 PT symptoms and improve vigour and cognitive and neuro-motor performance.
 XX
 PS Disclosure; Page 4; 21pp; English.
 XX
 CC The synthetic peptide is an example of a generic peptide whose sequence
 CC is based on the sequence of peptide T, a sub region of HIV gp120
 CC responsible for binding to brain membrane and human T cells. The peptide
 CC may be used for treatment of chronic fatigue syndrome not associated with
 CC HIV infection. The peptide will reduce fatigue, tension, anger and
 CC confusion and improves cognitive and neuromotor performance. See also
 CC AAR28918-42. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 5 AA;
 Query Match 61.5%; Score 16; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNFS 5
 Db ||:: 2 DNYT 5
 RESULT 10
 AAR44338
 ID AAR44338 standard; peptide; 5 AA.
 XX
 AC AAR44338;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-JUN-1994 (first entry)
 XX
 DE Peptide T related peptide for treating inflammation.
 XX
 KW Inflammation; antiinflammatory; immunomodulator; HTLV-1;
 KW multiple sclerosis; myopathy; chronic fatigue syndrome; toxic shock;
 KW arthritis; inflammatory bowel disease; host-versus-graft;
 KW graft-versus-host; transplant.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FH Modified-site 1..5
 FT /note= "one or more residues may be glycosylated"
 FT
 XX
 PN W09320102-A1.
 XX
 PD 14-OCT-1993.
 XX
 XX 29-MAR-1993; 93WO-GB000649.
 PF
 XX 27-MAR-1992; 92US-00858832.
 PR 14-MAY-1992; 92DK-00000645.
 PR 17-JUL-1992; 92US-00915118.
 PR 09-DEC-1992; 92US-00987674.
 XX
 XX (PEPT-) PEPTIDE TECHNOLOGY LTD.
 PA (DRUG-) DRUG ROYALTY CORP.
 XX
 XX Andersen AJ, Aston R, Carlen PL, Doob PR, Macfadden DK;
 PI Phipps DJ, Rathjen D, Widmer F;
 XX
 XX WPI; 1993-336832/42.
 DR
 XX New linear and cyclic peptide T analogues - used for treatment and
 PT prevention of inflammation, e.g. multiple sclerosis and myelopathies.
 XX
 PS Claim 7; Page 83; 103pp; English.
 XX

CC The invention relates to a group of linear or cyclic tetra- to deca-
 CC peptides which include Peptide T and its analogues, where at least one of
 CC the amino acids may optionally have a monomeric or polymeric carbohydrate
 CC substituted onto a hydroxyl, amino and/or amido group. In one aspect the
 CC invention relates to the use of these peptides for the treatment of
 CC inflammation; and in another aspect it relates to those peptides in which
 CC the carbohydrate moiety is present (other than glycosylated Prototype
 CC Peptide T) as new chemical entities. The present peptide is one of 10
 CC specific peptides listed in a sub-claim for use in the treatment of
 CC inflammation. The peptides act as immunomodulators in the treatment and
 CC prevention of inflammation. In particular they can be used in the
 CC treatment of multiple sclerosis, myopathies (including HTLV-1 associated
 CC myopathies) and symptoms and diseases associated with chronic immune
 CC activation including chronic fatigue syndrome, toxic shock, arthritis,
 CC inflammatory bowel disease, and host-versus-graft and graft-versus-host
 CC responses in transplant recipients. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 5 AA;
 Query Match 61.5%; Score 16; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNFS 5
 Db ||:: 2 DNYT 5

RESULT 11
 AAR59489
 ID AAR59489 standard; peptide; 5 AA.
 XX
 AC AAR59489;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-NOV-1995 (first entry)
 XX
 DE Peptide T variant used for treating eczema.
 XX
 KW Peptide T; prototype; octapeptide; eczema; dermatitis.
 KW
 XX Synthetic.
 XX
 PN W09508338-A1.
 XX
 PD 30-MAR-1995.
 XX
 PF 26-SEP-1994; 94WO-AU000574.
 XX
 PR 24-SEP-1993; 93AU-00001449.
 XX
 XX (PEPT-) PEPTIDE TECHNOLOGY LTD.
 PA
 XX Michaelis J, Trigg TE;
 PI
 XX WPI; 1995-139385/18.
 DR
 XX Treatment or prevention of eczema or dermatitis, esp. atopic eczema -
 PT using specified peptide, e.g the octapeptide Peptide T.
 PT
 XX Claim 3; Page 15; 20pp; English.
 PS
 XX The invention relates to a new method of treating eczema or dermatitis
 CC using Peptide T and its variants. The present sequence represents one of
 CC the preferred variants. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 5 AA;
 Query Match 61.5%; Score 16; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
DB ||::
2 DNYT 5

RESULT 12

AAR61484
ID AAR61484 standard; peptide; 5 AA.

XX AC AAR61484;
XX AC

DT 25-MAR-2003 (revised)
DT 26-NOV-1995 (first entry)

XX XX

DE Peptide T variant for use in treating Crohn's disease.

XX peptide T; prototype; Crohn's disease; ulcerative; colitis.
XX Synthetic.

OS

XX WO9508339-A1.

XX 30-MAR-1995.

XX 26-SEP-1994; 94WO-AU000575.
XX PR

XX 24-SEP-1993; 93AU-00001448.
XX XX

XX (PEPT-) PEPTIDE TECHNOLOGY LTD.
XX PA

XX Michaelis J, Sleight MJ;
XX PI

XX WPI; 1995-139386/18.
XX DR

XX Treatment or prevention of Crohn's disease or ulcerative colitis - by use
XX of specified peptide, e.g. Peptide T.

XX Claim 3; Page 15; 24pp; English.
XX PS

XX The invention relates to a new method of treating or preventing Crohn's
XX disease and/or ulcerative colitis using Peptide T and its variants. The
XX present sequence is one of the preferred peptides. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX CC

XX Sequence 5 AA;

Query Match 61.5%; Score 16; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 1.8e+06;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5

DB ||::

2 DNYT 5

RESULT 13

AAR75581
ID AAR75581 standard; peptide; 5 AA.

XX AC AAR75581;
XX AC

DT 06-MAR-1996 (first entry)
DT XX

XX gp120 binding Fab VH CDR1 #7.
XX DE

XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
XX 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
XX immunoreaction; neutralisation; passive immunotherapy.
XX OS

XX Synthetic.
XX XX

XX WO9511317-A1.
XX PN

PD 27-APR-1995.

XX 19-OCT-1994; 94WO-US011907.
XX PF

XX 19-OCT-1993; 93US-00139409.
XX PR

XX 26-APR-1994; 94US-00233619.
XX PR

XX 19-SEP-1994; 94US-00308841.
XX XX

XX (SCRI) SCRIPPS RES INST.
XX PA

XX Barbas CF, Burton DR, Lerner RA;
XX PI

XX WPI; 1995-170235/22.
XX DR

XX Synthetic human neutralising monoclonal antibodies to human
XX immunodeficiency virus - used for diagnosis and immunotherapy of HIV-
XX induced disease.

XX Example 2; Fig 5; 249pp; English.

XX The sequences given in AAR75575-94 represent complementarity determining
XX region 1 (CDR1) from various mutagenised human Fab's which comprise a
XX variable chain heavy regions (VH), which bind to HIV gp120. The Fab's are
XX based on the Fab MT4 and have the same amino acid composition as MT4 but
XX have randomised amino acids in the entire CDR1 and in four of the 18
XX amino acid residues in CDR3 (see also AAR75596-603). These Fab's are used
XX in the production of a human monoclonal antibody (MAB) which is capable of
XX of immunoreacting with, and neutralising HIV. The MAB's are capable of
XX reducing HIV infectivity titre in an in vitro virus infectivity assay by
XX 50% at a concentration of <100 ng of antibody per ml. They can be used to
XX provide passive immunotherapy to HIV in a human. They neutralise HIV more
XX effectively than antibodies selected from non-randomised combinatorial
XX libraries
XX CC

XX Sequence 5 AA;

Query Match 61.5%; Score 16; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5

DB ||::

1 NFS 3

RESULT 14

AAR75592
ID AAR75592 standard; peptide; 5 AA.

XX AC AAR75592;
XX AC

DT 06-MAR-1996 (first entry)
DT XX

XX gp120 binding Fab VH CDR1 #18.
XX DE

XX Human; Fab; variable chain; heavy; light; region; VH; VL; HIV; gp120;
XX 3b1; 3b3; 3b4; 3b9; MT4; humanised; monoclonal antibody; Mab;
XX immunoreaction; neutralisation; passive immunotherapy.
XX OS

XX Synthetic.
XX XX

XX WO9511317-A1.
XX PN

XX 27-APR-1995.
XX PD

XX 19-OCT-1994; 94WO-US011907.
XX PF

XX 19-OCT-1993; 93US-00139409.
XX PR

XX 26-APR-1994; 94US-00233619.
XX PR

XX 19-SEP-1994; 94US-00308841.
XX PR

XX (SCRI) SCRIPPS RES INST.
XX PA

```

PI  Barbas CF, Burton DR, Lerner RA;
XX
XX  WPI; 1995-170235/22.
XX
XX  Synthetic human neutralising monoclonal antibodies to human
PT  immunodeficiency virus - used for diagnosis and immuno:therapy of HIV-
PT  induced disease.
XX
XX
XX  Example 2; Fig 5; 249pp; English.
XX
XX  The sequences given in AAR75575-94 represent complementarity determining
CC  region 1 (CDR1) from various mutagenised human Fab's which comprise a
CC  variable chain heavy regions (VH), which bind to HIV gp120. The Fab's are
CC  based on the Fab M74 and have the same amino acid composition as M74 but
CC  have randomised amino acids in the entire CDR1 and in four of the 18
CC  amino acid residues in CDR3 (see also AAR75596-603). These Fab's are used
CC  in the production of a human monoclonal antibody (MAB) which is capable
CC  of immunoreacting with, and neutralising HIV. The MAB's are capable of
CC  reducing HIV infectivity titre in an in vitro virus infectivity assay by
CC  50% at a concentration of <100 ng of antibody per ml. They can be used to
CC  provide passive immunotherapy to HIV in a human. They neutralise HIV more
CC  effectively than antibodies selected from non-randomised combinatorial
CC  libraries
XX
XX  Sequence 5 AA;
XX
XX  Query Match      61.5%; Score 16; DB 2; Length 5;
XX  Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY      3 NFS 5
XX          |||
XX          1 NFS 3
XX
XX
XX  RESULT 15
XX  AAR97812
XX  ID      AAR97812 standard; peptide; 5 AA.
XX  AC      AAR97812;
XX  DT      22-AUG-1996 (first entry)
XX  DE      Vasoactive Intestinal Peptide VIP(7-11), for dermal ulcer treatment.
XX  KW      Vasoactive intestinal peptide; VIP; vasodilation; hyperkinemic; skin;
XX  KW      burn; decubitis; diabetes; ulcer; bedsores; pressure sore.
XX  OS      Synthetic.
XX  PN      JP08040926-A.
XX  PD      13-FEB-1996.
XX  PF      03-AUG-1994; 94JP-00182457.
XX  PR      03-AUG-1994; 94JP-00182457.
XX  PA      (YAKU-) YAKURIGAKU CHUO KENKYUSHO KK.
XX  DR      WPI; 1996-157021/16.
XX
XX  PT      Remedy for dermal ulcer - comprises vasoactive intestinal polypeptide as
XX  PT      active component.
XX
XX  PS      Claim 2; Page; 4pp; Japanese.
XX
XX  CC      Vasoactive intestinal peptide and related compounds are known to have
XX  CC      strong vasodilatory activity. They have now been found to be effective in
XX  CC      the treatment of skin ulcers, esp. decubitus ulcers but also burn ulcers,
XX  CC      diabetic ulcers, etc. VIP(1-28) is the preferred peptide for use in the
XX  CC      novel skin ulcer remedy, but the related compounds VIP(1-12), VIP(7-11),
XX  CC      VIP(10-28) and VIP(7-11, Thr8) are also suitable

```

```

XX  SQ      Sequence 5 AA;
XX
XX  Query Match      61.5%; Score 16; DB 2; Length 5;
XX  Best Local Similarity 50.0%; Pred. No. 1.8e+06;
XX  Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX  QY      2 DNFS 5
XX          |||
XX          2 DNYT 5
XX
XX  Search completed: September 10, 2005, 01:12:06
XX  Job time : 166 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 01:15:05 ; Search time 159 Seconds
(without alignments)
12.404 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 16569

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	26	100.0	5	16	US-10-795-795-12
3	19	73.1	5	15	US-10-436-549-13
4	19	73.1	5	16	US-10-712-425-13
5	19	73.1	5	17	US-10-808-187-2261
6	19	73.1	5	17	US-10-773-032-13
7	19	73.1	5	18	US-10-807-807-2261
8	19	73.1	5	11	US-09-855-604-905
9	18	69.2	5	12	US-09-855-604-905
10	17	65.4	5	10	US-09-788-006-163
11	16	61.5	5	10	US-09-788-006-161

12	61.5	5	10	US-09-788-006-162	Sequence 162, App
13	61.5	5	10	US-09-315-355-37	Sequence 37, Appl
14	61.5	5	11	US-09-943-944E-27	Sequence 27, Appl
15	61.5	5	14	US-10-006-869-242	Sequence 242, App
16	61.5	5	14	US-10-006-869-1725	Sequence 1725, Ap
17	61.5	5	15	US-10-395-032-242	Sequence 242, App
18	61.5	5	15	US-10-395-032-1725	Sequence 1725, Ap
19	61.5	5	15	US-10-182-058A-3	Sequence 3, Appl
20	61.5	5	15	US-10-182-058A-23	Sequence 23, Appl
21	61.5	5	17	US-10-808-187-1075	Sequence 1075, Ap
22	61.5	5	18	US-10-848-572-37	Sequence 37, Appl
23	61.5	5	18	US-10-807-807-1075	Sequence 1075, Ap
24	57.7	5	9	US-09-910-059-29	Sequence 29, Appl
25	57.7	5	14	US-10-006-869-323	Sequence 323, App
26	57.7	5	14	US-10-006-869-2134	Sequence 2134, App
27	57.7	5	14	US-10-315-515-146	Sequence 146, App
28	57.7	5	15	US-10-395-032-323	Sequence 323, App
29	57.7	5	15	US-10-395-032-2134	Sequence 2134, Ap
30	57.7	5	15	US-10-395-607-137	Sequence 197, App
31	57.7	5	16	US-10-798-380-104	Sequence 104, App
32	57.7	5	17	US-10-855-013-13	Sequence 13, Appl
33	53.8	5	9	US-09-982-172-40	Sequence 40, Appl
34	53.8	5	14	US-10-006-869-322	Sequence 322, App
35	53.8	5	14	US-10-206-699-44	Sequence 44, Appl
36	53.8	5	15	US-10-395-032-322	Sequence 322, App
37	53.8	5	15	US-10-436-549-585	Sequence 585, App
38	53.8	5	15	US-10-377-134-89	Sequence 89, Appl
39	53.8	5	16	US-10-416-249-624	Sequence 624, App
40	53.8	5	16	US-10-416-249-628	Sequence 628, App
41	53.8	5	16	US-10-712-425-585	Sequence 585, App
42	53.8	5	17	US-10-808-187-561	Sequence 561, App
43	53.8	5	17	US-10-728-246-22	Sequence 22, Appl
44	53.8	5	17	US-10-773-032-585	Sequence 585, App
45	53.8	5	17	US-10-684-346-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-09-911-1298-12
; Sequence 12, Application US/099111298
; Publication No. US20030040600A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,1298
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-1298-12

Query Match 100.0%; Score 26; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNFS 5
DB 1 LDNFS 5

RESULT 2
US-10-795-795-12
; Sequence 12, Application US/10795795
; Publication No. US20040186271A1
; GENERAL INFORMATION:

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; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-795-795-12

Query Match          100.0%; Score 26; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDNFS 5
Db      1 LDNFS 5

RESULT 3
US-10-436-549-13
; Sequence 13, Application US/10436549
; Publication No. US20040038307A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Dr. Xun
; APPLICANT: Chan, John W.
; APPLICANT: Zhang, Shengsheng
; APPLICANT: Benkovic, Stephen J.
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
; FILE REFERENCE: ENGE-P01-001
; CURRENT APPLICATION NUMBER: US/10/436,549
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,626
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/433,319
; PRIOR FILING DATE: 2002-12-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-712-425-13

Query Match          73.1%; Score 19; DB 16; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
Db      1 DNFS 4

RESULT 5
US-10-808-187-2261
; Sequence 2261, Application US/10808187
; Publication No. US2005000909A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
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; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-2261

Query Match      73.1%; Score 19; DB 17; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
DB      2 DNFA 5

RESULT 6
US-10-773-032-13
; Sequence 13, Application US/10773032
; Publication No. US20050069911a1
; GENERAL INFORMATION:
; APPLICANT: MENG, XUN
; APPLICANT: AFEYAN, NOUBAR B.
; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN
; FILE REFERENCE: ENGE-P03-001
; CURRENT APPLICATION NUMBER: US/10/773,032
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: 10/712,425
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 10/436,549
; PRIOR FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,626
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,197
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-773-032-13

Query Match      73.1%; Score 19; DB 17; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
DB      1 DNFA 4

RESULT 7
US-10-807-807-2261
; Sequence 2261, Application US/10807807
; Publication No. US20050181357a1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2261
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-2261

Query Match      73.1%; Score 19; DB 18; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 DNFS 5
DB      2 DNFA 5

RESULT 8
US-09-855-604-905
; Sequence 905, Application US/09855604
; Publication No. US20040214165a1
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: FORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
```

APPLICANT: GUIGUENO, AGNES
APPLICANT: GOGUET DE LA SALMONIERE, YVES
TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
TITLE OF INVENTION: PREVENTING TUBERCULOSIS
FILE REFERENCE: 03715.0062-01000
CURRENT APPLICATION NUMBER: US/09/855,604
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/485,536
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/FR98/01813
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: FR 97 10404
PRIOR FILING DATE: 1997-08-14
PRIOR APPLICATION NUMBER: FR 97 11325
PRIOR FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 935
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 905
LENGTH: 5
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-855-604-905

Query Match 69.2%; Score 18; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
Db 3 DNF 5

RESULT 9
US-09-855-604-905
Sequence 905 Application US/09855604
Publication No. US2005015871A9
GENERAL INFORMATION:
APPLICANT: GICQUEL, BRIGITTE
APPLICANT: PORTNOI, DENIS
APPLICANT: LIM, ENG-MONG
APPLICANT: PELICIC, VLADIMIR
APPLICANT: GUIGUENO, AGNES
APPLICANT: GOGUET DE LA SALMONIERE, YVES
TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
TITLE OF INVENTION: PREVENTING TUBERCULOSIS
FILE REFERENCE: 03715.0062-01000
CURRENT APPLICATION NUMBER: US/09/855,604
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/485,536
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/FR98/01813
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: FR 97 10404
PRIOR FILING DATE: 1997-08-14
PRIOR APPLICATION NUMBER: FR 97 11325
PRIOR FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 935
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 905
LENGTH: 5
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-09-855-604-905

Query Match 69.2%; Score 18; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
Db 3 DNF 5

RESULT 10
US-09-788-006-163
Sequence 163 Application US/09788006
Publication No. US20030036093A1
GENERAL INFORMATION:
APPLICANT: Floudas, Christopher A.
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REFERENCE: PU-0007
CURRENT APPLICATION NUMBER: US/09/788,006
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
SEQ ID NO 163
LENGTH: 5
TYPE: PRT
ORGANISM: Hordeum vulgare
US-09-788-006-163

Query Match 65.4%; Score 17; DB 10; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNFS 5
Db 1 LDNIA 5

RESULT 11
US-09-788-006-161
Sequence 161 Application US/09788006
Publication No. US20030036093A1
GENERAL INFORMATION:
APPLICANT: Floudas, Christopher A.
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REFERENCE: PU-0007
CURRENT APPLICATION NUMBER: US/09/788,006
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
SEQ ID NO 161
LENGTH: 5
TYPE: PRT
ORGANISM: Hordeum vulgare
US-09-788-006-161

Query Match 61.5%; Score 16; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDN 3
Db 3 LDN 5

RESULT 12
US-09-788-006-162
Sequence 162 Application US/09788006
Publication No. US20030036093A1
GENERAL INFORMATION:
APPLICANT: Floudas, Christopher A.
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REFERENCE: PU-0007
CURRENT APPLICATION NUMBER: US/09/788,006
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 162
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-788-006-162

Query Match      61.5%; Score 16; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDN 3
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Db      2 LDN 4

RESULT 13
US-09-315-355-37
; Sequence 37, Application US/09315355
; Publication No. US20030157482A1
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; DETECTION OF CERVICAL CANCER
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,355
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GREENHALGH, DUNCAN A
; REGISTRATION NUMBER: 38,678
; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-315-355-37

Query Match      61.5%; Score 16; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDN 3
      |||
Db      1 LDN 3

RESULT 14
US-09-943-944E-27
; Sequence 27, Application US/09943944E
; Publication No. US20040014036A1
; GENERAL INFORMATION:
; APPLICANT: Ptashne, et al.,
; TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses
; FILE REFERENCE: 0342941-0065
; CURRENT APPLICATION NUMBER: US/09/943,944E
; CURRENT FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Random peptide
US-09-943-944E-27

Query Match      61.5%; Score 16; DB 11; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDNF 4
      |||
Db      2 LDTF 5

RESULT 15
US-10-006-869-242
; Sequence 242, Application US/10006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C7
; CURRENT APPLICATION NUMBER: US/10/006,869
; CURRENT FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 242
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; cadherin-8 cell adhesion recognition sequence
US-10-006-869-242

Query Match      61.5%; Score 16; DB 14; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 LDNFS 5
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Db      1 LBEFS 5

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Job time : 161 secs
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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:18:31 ; Search time 64 Seconds
(without alignments)
60.431 Million cell updates/sec

Title: US-10-795-795-6

Perfect score: 55

Sequence: 1 WEYFIAAEV 10

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Total number of hits satisfying chosen parameters: 135071

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	26	47.3	10	1 AAP30391	Aap30391 Gonadotro
8	26	47.3	10	1 AAP50839	Aap50839 Sequence
9	26	47.3	10	1 AAP50509	Aap50509 Sequence
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11	26	47.3	10	1 AAP71492	Aap71492 LH-RH pep
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13	26	47.3	10	1 AAP71233	Aap71233 Lutensini
14	26	47.3	10	1 AAP71232	Aap71232 Lutensini
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17	26	47.3	10	2 AAR23954	Aar23954 LH-RH, so
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19	26	47.3	10	2 AAR76209	Aar76209 LH-RH ana
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23	26	47.3	10	2 AAY46210	Aay46210 Immunogen
24	26	47.3	10	2 AAY00814	Aay00814 HLA-A24 a
25	26	47.3	10	5 ABG65741	Abg65741 Plant ICK

ALIGNMENTS

RESULT 1

ABU62020

ID ABU62020 standard; peptide; 10 AA.

XX AC ABU62020;

XX XX 26-AUG-2003 (first entry)

XX XX Human blood coagulation factor Va peptide, AP4.

XX KW Human; blood coagulation factor Va; blood clotting factor Va;

KW prothrombinase inhibition; prothrombinase-inhibiting peptide;

KW blood clotting disorder; thrombotic disorder; blood clot formation;

KW blood vessel obstruction; coronary artery disease; unstable angina;

KW valvular heart disease; stroke; blood anticoagulation; anticoagulant.

KW atrial fibrillation; stroke; blood anticoagulation; anticoagulant.

XX OS Homo sapiens.

XX XX US2003040600-A1.

XX XX 27-FEB-2003.

XX PF 23-JUL-2001; 2001US-00911129.

XX PR 23-JUL-2001; 2001US-00911129.

XX PA (KALA/) KALAFATIS M.

XX PA (MANN/) MANN K.

XX PI Kalafatis M, Mann K;

XX DR WPI; 2003-492177/46.

XX XX Novel anticoagulant peptide derived from the amino acid region 307-356 of

PT human blood clotting factor Va, useful for preventing thrombotic

PT disorders resulting from formation of blood clots that obstruct blood

XX vessels.

XX PS Claim 10; Fig 2; 20pp; English.

XX CC The present invention relates to peptides derived from human blood

CC coagulation (clotting) factor Va which exhibit inhibition of

CC prothrombinase. A pharmaceutical composition comprising one or more of

CC the prothrombinase-inhibiting peptides may be used for treating human

CC subjects with blood clotting disorders. The peptides are useful for

CC preventing thrombotic disorders resulting from the formation of blood

CC clots that obstruct blood vessels, e.g. due to a condition chosen from

Ade67361 Human 161
Ade67607 Human 161
Ade66447 Human 161
Ade69879 Human 161
Ade67158 Human 161
Ade66601 Human 161
Ade66908 Human 161
Ade66356 Human 161
Ade66436 Human 161
Ade69372 Human 161
Ade69670 Human 161
Ade69995 Human 161
Ade67100 Human 161
Ade69994 Human 161
Ade69796 Human 161
Ade69821 Human 161
Ade69261 Human 161
Ade69848 Human can
Adk10717 Human pap
Adk10716 Human pap

CC coronary artery disease, valvular heart disease, stable and unstable
 CC angina, myocardial infarction, atrial fibrillation and stroke. The
 CC peptides of the invention exhibit an IC50 of between 50 nanoM-500 microM
 CC for inhibition of prothrombinase. The peptides exhibit excellent blood
 CC anticoagulation properties with little or no adverse side effects. The
 CC present sequence represents a peptide that inhibits prothrombinase
 CC activity
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYFIAAEV 10
 |||||
 Db 1 WEYFIAAEV 10

RESULT 2

ADS64542
 ID ADS64542 standard; peptide; 10 AA.

XX
 AC ADS64542;

DT 16-DEC-2004 (first entry)

DE Human blood coagulation factor Va peptide, AP4.

XX Prothrombinase inhibitor; human; blood coagulation factor Va;
 KW blood clotting disorder; thrombotic disorder; thrombolytic.
 KW
 XX Homo sapiens.

XX US2004186271-A1.
 PN
 XX
 XX 23-SEP-2004.

PF 08-MAR-2004; 2004US-00795795.

XX 23-JUL-2001; 2001US-00911129.

XX (KALA/) KALAFATIS M.
 PA (MANN/) MANN K G.

XX Kalafatis M, Mann KG;

XX WPI; 2004-689241/67.

XX New prothrombinase-inhibiting peptide derived from a specific amino acid
 PT sequence of human blood coagulation factor Va, useful for treating human
 PT subjects with blood clotting disorders.

XX Claim 10; SEQ ID NO 6; 20pp; English.

XX The present invention relates to a prothrombinase-inhibiting peptide
 CC derived from a specific amino acid sequence of human blood coagulation
 CC factor Va. The invention is useful for treating human subjects with blood
 CC clotting disorders. The invention is also useful for preventing
 CC thrombotic disorders resulting from formation of blood clots that
 CC obstructs blood vessels. The present sequence is the human blood
 CC coagulation factor Va peptide.

XX Sequence 10 AA;

Query Match 100.0%; Score 55; DB 8; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYFIAAEV 10
 |||||
 Db 1 WEYFIAAEV 10

RESULT 3

ABU62019
 ID ABU62019 standard; peptide; 10 AA.

XX
 AC ABU62019;

XX 26-AUG-2003 (first entry)

DE Human blood coagulation factor Va peptide, AP3.

XX Human; blood coagulation factor Va; blood clotting factor Va;
 KW prothrombinase inhibition; prothrombinase-inhibiting peptide;
 KW blood clotting disorder; thrombotic disorder; blood clot formation;
 KW blood vessel obstruction; coronary artery disease; unstable angina;
 KW valvular heart disease; stable angina; myocardial infarction;
 KW atrial fibrillation; stroke; blood anticoagulation; anticoagulant.

XX Homo sapiens.

XX US2003040600-A1.

XX 27-FEB-2003.

XX 23-JUL-2001; 2001US-00911129.

XX 23-JUL-2001; 2001US-00911129.

XX (KALA/) KALAFATIS M.

PA (MANN/) MANN K.

XX Kalafatis M, Mann K;

XX WPI; 2003-492177/46.

XX Novel anticoagulant peptide derived from the amino acid region 307-356 of
 PT human blood clotting factor Va, useful for preventing thrombotic
 PT disorders resulting from formation of blood clots that obstruct blood
 PT vessels.

XX Claim 10; Fig 2; 20pp; English.

XX The present invention relates to peptides derived from human blood
 CC coagulation (clotting) factor Va which exhibit inhibition of
 CC prothrombinase. A pharmaceutical composition comprising one or more of
 CC the prothrombinase-inhibiting peptides may be used for treating human
 CC subjects with blood clotting disorders. The peptides are useful for
 CC preventing thrombotic disorders resulting from the formation of blood
 CC clots that obstruct blood vessels, e.g. due to a condition chosen from
 CC coronary artery disease, valvular heart disease, stable and unstable
 CC angina, myocardial infarction, atrial fibrillation and stroke. The
 CC peptides of the invention exhibit an IC50 of between 50 nanoM-500 microM
 CC for inhibition of prothrombinase. The peptides exhibit excellent blood
 CC anticoagulation properties with little or no adverse side effects. The
 CC present sequence represents a peptide that inhibits prothrombinase
 CC activity

XX Sequence 10 AA;

Query Match 60.0%; Score 33; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYFI 5
 |||||
 Db 6 WEYFI 10

RESULT 4

ADS64541
 ID ADS64541 standard; peptide; 10 AA.

XX
 AC ADS64541;

XX DT 16-DEC-2004 (first entry)
XX DE Human blood coagulation factor Va peptide, AP3.
XX KW Prothrombinase inhibitor; human; blood coagulation factor Va;
XX KW blood clotting disorder; thrombotic disorder; thrombolytic.
XX OS Homo sapiens.
XX PN US2004186271-A1.
XX PD 23-SEP-2004.
XX PF 08-MAR-2004; 2004US-00795795.
XX PR 23-JUL-2001; 2001US-00911129.
XX PA (KALA/) KALAFATIS M.
XX PA (MANN/) MANN K G.
XX PI Kalafatis M, Mann KG;
XX DR WPI; 2004-689241/67.
XX SQ New prothrombinase-inhibiting peptide derived from a specific amino acid
PT sequence of human blood coagulation factor Va, useful for treating human
PT subjects with blood clotting disorders.
XX PS Claim 10; SEQ ID NO 5; 20pp; English.
XX CC The present invention relates to a prothrombinase-inhibiting peptide
CC derived from a specific amino acid sequence of human blood coagulation
CC factor Va. The invention is useful for treating human subjects with blood
CC clotting disorders. The invention is also useful for preventing
CC thrombotic disorders resulting from formation of blood clots that
CC obstructs blood vessels. The present sequence is the human blood
CC coagulation factor Va peptide.
XX SQ Sequence 10 AA;
Query Match 60.0%; Score 33; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WEYFI 5
Db 6 WEYFI 10
RESULT 5
ID ABG65739 standard; peptide; 10 AA.
XX AC ABG65739;
XX DT 27-AUG-2002 (first entry)
XX DE Plant ICK protein conserved motif 1 #47.
XX KW Plant; inhibitor of cyclin dependent kinase; ICK.
XX OS Oryza sativa.
XX PN WO200228893-A2.
XX PD 11-APR-2002.
XX PF 29-JUN-2001; 2001WO-IB001492.
XX PR 14-JUL-2000; 2000US-0218471P.
XX PR 13-OCT-2000; 2000US-0241219P.
XX

PA (CROP-) CROPDESIGN NV.
XX Frankard VMS, Peres Bota AM, Droual A, Mironov V, Inze D;
PI Hatzfeld Y;
XX WPI; 2002-471311/50.
XX Novel plant ICK (Inhibitors of Cyclin Dependent Kinases) polypeptide used
PT to screen substrates, drugs or compounds which modulate ICK activity and
PT treat disorders characterized by an insufficient or excessive production
PT of ICK inhibitors.
XX Disclosure; Page 14; 141pp; English.
XX This invention relates to the DNA and protein sequences of novel isolated
CC ICK (Inhibitors of Cyclin Dependent Kinases) proteins. The sequences of
CC the invention may be used for treating disorders characterised by
CC insufficient or excessive production of an ICK inhibitor. The protein of
CC the invention may also be used to screen for naturally-occurring ICK
CC substrates, drugs or compounds which modulate ICK activity, as well as to
CC treat disorders characterised by insufficient or excessive production of
CC ICK protein, forms which have decreased or aberrant activity compared to
CC ICK wild type protein. The present sequence represents an inhibitor of
CC cyclin dependent kinase (ICK) protein of the invention
XX SQ Sequence 10 AA;
Query Match 49.1%; Score 27; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 EYFIAAE 9
Db 3 EAFFAAE 10
RESULT 6
ID AAP10167 standard; peptide; 10 AA.
XX AC AAP10167;
XX DT 25-MAR-2003 (revised)
DT 14-OCT-1992 (first entry)
XX Sequence of luteinizing hormone releasing hormone (LH-RH) antagonist.
XX Ovulation regulation; gonadotropin; luteinising hormone; antiovaratory;
KW follicle stimulating hormone; luteinising hormone releasing hormone.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /label= N-succinyl-D-Phe
FT Modified-site 2 /label= D-p-chloroPhe
FT Modified-site 3 /label= D-Trp
FT Modified-site 4 /label= Ser(O-benzyl)
FT Modified-site 6 /label= D-Phe
FT Modified-site 8 /label= Arg(NG-tosyl)
FT Modified-site 10 /note= "attached to benzhydrylamine resin"
XX GB2053229-A.
XX PN 04-FEB-1981.
XX PD 13-JUN-1979; 79CA-00329643.
XX

XX PR 13-JUN-1979; 79CA-00329643.
 PR 02-JUN-1980; 80US-00155249.
 PR 20-JAN-1982; 82US-00341137.
 XX
 XX (COYD/) COY D H.
 PA (SCHA/) SCHALLY A V.
 XX PI
 XX COY DH, Schally AV;
 XX WPI; 1981-08335D/06.
 XX Luteinising hormone-releasing hormone antagonist peptide(s) - useful e.g.
 PT as contraceptives, oestrus regulators and regulators of human menopausal
 PT gonadotropin.
 XX
 XX Example; Page 8; 13pp; English.
 XX AAP10165 is the generic sequence for peptides in compounds having LH-RH
 CC antagonising properties. They can be used to treat precocious puberty; and
 CC hormone dependent tumors; hirsutism; acne; amenorrhea; endometriosis; and
 CC ovarian and mammary cystic diseases. They are also useful for regulating
 CC ovulation and for regulating the human menopausal gonadotropin, follicle-
 CC stimulating hormone (FSH) and luteinizing hormone (LH). A dosage level
 CC that is in the range of from about 25 mcg per kilogram body weight is
 CC most desirably employed in order to achieve effective results. In the
 CC examples, solid phase synthesis is used to prepare specific examples of
 CC the generic compound (AAP10166-P10169). (Updated on 25-MAR-2003 to
 CC correct PR field.)
 XX SQ Sequence 10 AA;
 Query Match 47.3%; Score 26; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WEYFI 5
 Db 3 WSYFL 7
 RESULT 7
 AAP30391
 ID AAP30391 standard; peptide; 10 AA.
 XX AC AAP30391;
 XX 25-MAR-2003 (revised)
 DT 09-SEP-1992 (first entry)
 XX Gonadotropin-releasing hormone analogue.
 DE Luteinising; hormone; LH; contraceptives; mammary; carcinoma; prostate;
 KW cancer; aneostronic; anovulatory; follicular; cyst; cattle.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "pyro Glu"
 FT Misc-difference 6 /note= "D-4-chloro-Phe"
 FT Modified-site 10 /label= Gly-NH2
 FT
 XX WO8304250-A.
 XX 08-DEC-1983.
 PD 25-MAY-1982; 82HU-00001692.
 XX 25-MAY-1982; 82HU-00001692.

PA (RICT) RICHTER GEDEON VEGYESZETI GYAR.
 PA (ANTO/) ANTONI F.
 PA (MAGY) MTA KOEPPONTI HIVATA KI.
 PA (REAN-) REANAL FINOMVEGYSZERGYAR.
 XX
 XX Antoni F, Erchevyi J, Horvath A, Keri G, Mezo I, Mezo I;
 PI Nikolics K, Seprödi J;
 XX WPI; 1983-844749/50.
 DR
 XX Gonadotropin-releasing hormone analogues - useful for contraception,
 PT cancer therapy, etc.
 XX
 XX Claim 1; Page 17; 20pp; English.
 PS
 XX The peptide is a gonadotropin releasing hormone analogue having higher
 CC luteinising hormone releasing activity than the natural hormone. The
 CC peptide may be used in veterinary and human medicine e.g. as a
 CC contraceptive, for the treatment of mammary carcinoma or prostate cancer,
 CC as aneostronic or anovulatory agents for animals, or for treating
 CC follicular cysts in cattle. See also AAP30390. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX SQ Sequence 10 AA;
 Query Match 47.3%; Score 26; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WEYFI 5
 Db 3 WSYFL 7
 RESULT 8
 AAP50839
 ID AAP50839 standard; peptide; 10 AA.
 XX AC AAP50839;
 XX 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 01-NOV-1991 (first entry)
 XX Sequence of hormonal decapeptide deriv. used to induce release of eggs
 DE and sperm from fish.
 DE Hormone; reproductive; ovulation; spermatogenesis; fertility.
 XX Actinopterygii.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1 /label= pyroGlu
 FT Misc-difference 6 /label= D-Phe
 FT Modified-site 10 /label= Gly-NH2
 FT
 XX BE901308-A.
 XX 19-JUN-1985.
 PD 19-DEC-1984; 84BE-00901308.
 XX 23-DEC-1983; 83HU-00004457.
 XX (VALT-) KOEPPONTI VALTO ES HITELBANK RT.
 PA (KZBU-) KZBUTE.
 XX WPI; 1985-159469/27.
 XX

PT Inducing release of eggs and sperm from fish - out of the normal season,
 XX by treatment with hormonal decapeptide derivative.
 PS Disclosure; Page 8; 16pp; French.
 XX
 CC The peptides of the invention have hormonal activity for all species of
 CC fish, are active under widely differing conditions and, being synthetic,
 CC can be administered in precise doses (contrast the use of natural
 CC hypophyseal hormone extracted from carp). They are administered at a dose
 CC of 0.1 micrograms - 5 mg., esp. 5-100 micrograms. For fish which are not
 CC mature, 2-12 doses are given, the last dose being at least equal to
 CC (pref. 1.5 greater than) the preceding dose. (Updated on 10-MAR-2003 to
 CC add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYEFI 5
 |||:
 Db 3 WSYFL 7

RESULT 9
 AAP50509
 ID AAP50509 standard; protein; 10 AA.

XX
 AC AAP50509;

XX
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 01-NOV-1991 (first entry)

XX Sequence of gonadoliberin analogue.

DE Hormone; reproduction; fertility; contraception; ovulation.

XX
 KW Vertebrata.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Protein 1. .9
 FT /note= "also claimed with modified Pro(9) (=Pro-EA) "
 FT Misc-difference 1 /label= pyroglu
 FT Misc-difference 6 /label= D-Phe
 FT Modified-site 10 /label= Gly-NH2

XX BE901307-A.

XX 19-JUN-1985.

XX 19-DEC-1984; 84BE-00901307.

XX 23-DEC-1983; 83HU-00004458.

XX (VALT-) KOE2PONTI VALTO ES HITELBANK RT.
 PA (INNO-) INNOVACIOS ALAP.
 PA (KERT-) KERTZBUTE.

XX WPI; 1985-159468/27.

XX New gonadoliberin analogues - useful for ovulation control in fish birds
 PT and mammals.

XX Claim 2; Page 25; 29pp; French.

XX The analogues of the invention are useful for controlling ovulation in
 CC fish, birds and mammals. They have higher activity than their natural

CC counterparts. (Updated on 10-MAR-2003 to add missing OS field.) (Updated
 XX on 25-MAR-2003 to correct PA field.)
 SQ Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYEFI 5
 |||:
 Db 3 WSYFL 7

RESULT 10

AAP61418

ID AAP61418 standard; protein; 10 AA.

XX
 AC AAP61418;

XX 25-OCT-1991 (first entry)

XX Lutenising hormone releasing hormone antagonist.

XX LHRH; canine contraception; pyometritis; endometritis.

OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT /note= "N-Ac-D-Trp"
 FT Modified-site 2 /label= OTHER
 FT /note= "3-(p-Chlorophenyl)-D-alanyl"
 FT Modified-site 3 /label= D-Trp
 FT Modified-site 6 /label= D-Phe

XX EP199302-A.

XX 29-OCT-1986.

XX 18-APR-1986; 86EP-00105372.

XX 19-APR-1985; 85US-00725267.

XX (SYNT) SYNTEX (USA) .

XX Vickery BH;

XX WPI; 1986-286068/44.

XX Contraception in dogs using LHRH antagonists - for terminating heat and
 PT pregnancy and treating pyometritis and endometritis.

XX Claim 4; Page 17; 19pp; English.

XX The LHRH antagonists may be used to treat female dogs, terminating
 CC oestrus or pregnancy, and in treatment of pyometritis and endometritis.
 CC Treatment is useful when the date of conception is unknown, as it may be
 CC employed at any time during pregnancy, is well tolerated, reversible and
 CC avoids the use of steroids

XX Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 5.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYEFI 5
 |||:

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Db          3 WSYFL 7

RESULT 11
AAP71492
ID AAP71492 standard; peptide; 10 AA.
XX
AC AAP71492;
XX
DT 07-MAY-1991 (first entry)
XX
DE LH-RH peptide analogue.
XX
KW LH-RH analogue; oestrus; fertility.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6..6
FT /label= D-p-ethyl-phenylalanine
XX
PN DD248126-A.
XX
PD 29-JUL-1987.
XX
PF 20-AUG-1984; 84DD-00266440.
XX
PR 20-AUG-1984; 84DD-00266440.
XX
PA (BERC ) BERLIN CHEMIE VEB.
XX
PI Egler H, Walz H, Schwarz J, Bilk L, Flegel M, Krchnak V;
PI Krcjldlo M, Kolinsky J;
XX
DR WPI; 1987-349110/50.
XX
XX New LH-Rh nona-peptide or deca-peptide analogues - contg. D-P-ethyl-
PT phenylalanine residue in the 6-position, prepd. by a 3 plus 6 or 3 plus 7
PT solid phase synthesis.
XX
PS Claim; Page 1; 5pp; German.
XX
CC Glu1 is pGlu. The sequence may have residue G10 lacking. The analogue can
CC be used as oestrus synchronisation agent in veterinary medicine and in
CC the treatment of fertility disorders in human medicine. They are more
CC potent and longer acting than natural LH-RH
XX
SQ Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEYFI 5
Db | | | :
3 WSYFL 7

RESULT 12
AAP71168
ID AAP71168 standard; peptide; 10 AA.
XX
AC AAP71168;
XX
DT 10-MAR-2003 (revised)
DT 25-MAY-1991 (first entry)
XX
DE Sequence of luteinising hormone - follicle stimulating hormone analogue
DE (D-Phe 6) LH-RH.
XX
KW Breast cancer; prostate cancer; therapy; endometriosis;
KW benign prostatic hyperplasia.
XX

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OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /label= pyro-Glu
FT Misc-difference 6 /label= D-Phe
FT Misc-difference 10 /label= Gly-NH2
XX
XX CH661206-A.
XX
XX 15-JUL-1987.
XX
XX 23-SEP-1983; 83CH-00005187.
XX
XX 23-SEP-1983; 83CH-00005187.
XX
XX (DEBI-) DESIOPHARM SA..
XX
XX Tice TR, Orsolini P, Mauvernay RY, Schally AV;
XX
XX WPI; 1987-228660/33.
XX
XX Medicament for treating hormone-dependent diseases - comprises
PT luteinising hormone- releasing hormone microencapsulated in D,L-glycolide
PT -lactide copolymer.
XX
XX Claim 2; Page 2; 6pp; French.
XX
XX The patentors claim a medicament prepd. by microencapsulation of LH-RH or
CC synthetic analogue in a D,L-lactide/glycolide copolymer. The medicament
CC is used in treatment of eg, cancer of the breast or prostate,
CC endometriosis or benign prostatic hyperplasia. The coated compen. has
CC enhanced antagonistic effects c.f. corresp. uncoated doses. Doses are 0.1
CC -10 mcg/kg/day, pref. i.m. (Updated on 10-MAR-2003 to add missing OS
CC field.)
XX
XX SQ Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEYFI 5
Db | | | :
3 WSYFL 7

RESULT 13
AAP71233
ID AAP71233 standard; protein; 10 AA.
XX
AC AAP71233;
XX
DT 29-APR-1991 (first entry)
XX
XX Luteinising hormone releasing hormone analogue.
XX
XX Luteinising hormone releasing hormone; cancer; cytotoxic effects;
KW bone marrow; agonist; radiotherapy; chemotherapy;
KW (D-Phe1, D-p-CI-Phe2, D-Trp3, D-Phe6) -LHRH.
XX
XX Synthetic.
XX
XX CH659392-A.
XX
XX 30-JAN-1987.
XX
XX 07-MAY-1984; 84CH-00002226.
XX
XX 07-MAY-1984; 84CH-00002226.
XX

```

PA (DEBI-) DEBIOPHARM SA.
XX
PI Mathe G, Misset JL, Lemaigre G, Mauvernay RY, Schally AV;
XX
DR WPI; 1987-037621/06.
XX
XX Compns. inhibiting cytotoxic effects in cancer therapy - contain
PT luteinising and follicle stimulating hormone release hormone or its
PT analogues.
XX
PS Claim 2; Page 2; 4pp; English.
XX
CC The analogue is an antagonist. It inhibits the cytotoxic effects of
CC cancer therapy on bone marrow cells, and protects the cells from the
CC undesirable effects of radio- and chemotherapy used to treat hormone-
CC dependent and -independent cancers. The compns. may be in sustained
CC release form and may be given parenterally, esp. i.m
XX
SQ Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEYFI 5
Db 3 WSYFL 7

RESULT 14
AAP71232
ID AAP71232 standard; protein; 10 AA.
XX
AC AAP71232;
XX
XX 29-APR-1991 (first entry)
XX
XX Luteinising hormone releasing hormone analogue.
XX
KW Luteinising hormone releasing hormone;
KW (D-Phe2, D-Trp3, D-Phe6)-LHRH cytotoxic effects; bone marrow; agonist;
KW radiotherapy; chemotherapy; cancer.
XX
OS Synthetic.
XX
PN CH659392-A.
XX
PD 30-JAN-1987.
XX
XX 07-MAY-1984; 84CH-00002226.
XX
XX 07-MAY-1984; 84CH-00002226.
XX
XX (DEBI-) DEBIOPHARM SA.
XX
XX Mathe G, Misset JL, Lemaigre G, Mauvernay RY, Schally AV;
XX WPI; 1987-037621/06.
XX
XX Compns. inhibiting cytotoxic effects in cancer therapy - contain
PT luteinising and follicle stimulating hormone release hormone or its
PT analogues.
XX
PS Claim 2; Page 2; 4pp; English.
XX
CC The analogue is an antagonist. It inhibits the cytotoxic effects of
CC cancer therapy on bone marrow cells, and protects the cells from the
CC undesirable effects of radio- and chemotherapy used to treat hormone-
CC dependent and -independent cancers. The compns. may be in sustained
CC release form and may be given parenterally, esp. i.m
XX
SQ Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEYFI 5
Db 3 WSYFL 7

RESULT 15
AAP71230
ID AAP71230 standard; protein; 10 AA.
XX
AC AAP71230;
XX
XX 29-APR-1991 (first entry)
XX
XX Luteinising hormone releasing hormone analogue.
XX
KW Luteinising hormone releasing hormone; (D-Phe6, Az Gly-NH2 10)-LHRH;
KW cytotoxic effects; bone marrow; agonist; radiotherapy; chemotherapy;
KW cancer.
XX
OS Synthetic.
XX
PN CH659392-A.
XX
PD 30-JAN-1987.
XX
XX 07-MAY-1984; 84CH-00002226.
XX
XX 07-MAY-1984; 84CH-00002226.
XX
XX (DEBI-) DEBIOPHARM SA.
XX
XX Mathe G, Misset JL, Lemaigre G, Mauvernay RY, Schally AV;
XX WPI; 1987-037621/06.
XX
XX Compns. inhibiting cytotoxic effects in cancer therapy - contain
PT luteinising and follicle stimulating hormone release hormone or its
PT analogues.
XX
PS Claim 2; Page 2; 4pp; English.
XX
CC The analogue is an agonist. It inhibits the cytotoxic effects of cancer
CC therapy on bone marrow cells, and protects the cells from the undesirable
CC effects of radio- and chemotherapy used to treat hormone- dependent and -
CC independent cancers. The compns. may be in sustained release form and
CC may be given parenterally, esp. i.m
XX
SQ Sequence 10 AA;

Query Match 47.3%; Score 26; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WEYFI 5
Db 3 WSYFL 7

Search completed: September 10, 2005, 00:54:49
Job time : 65 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:54:07 ; Search time 482 Seconds
(without alignments)
24.232 Million cell updates/sec

Title: US-10-795-795-6

Perfect score: 55

Sequence: 1 WYFIAAEV 10

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 172348

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main.*
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37: /cgn2_6/ptodata/1/paa/US60 COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	55	100.0	10	33	US-10-795-795-6
2	33	60.0	10	33	US-10-795-795-5
3	27	49.1	10	35	US-10-937-912-105
4	26	47.3	10	7	US-08-347-610-236
5	26	47.3	10	7	US-08-347-610-237
6	26	47.3	10	7	US-08-347-610-252
7	26	47.3	10	7	US-08-347-610A-236
8	26	47.3	10	7	US-08-347-610A-237
9	26	47.3	10	7	US-08-347-610A-252
10	26	47.3	10	7	US-08-347-610B-236
11	26	47.3	10	7	US-08-347-610B-237
12	26	47.3	10	7	US-08-347-610B-252
13	26	47.3	10	7	US-08-347-610C-236
14	26	47.3	10	7	US-08-347-610C-237
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16	26	47.3	10	18	US-09-458-298-50
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18	26	47.3	10	18	US-09-458-298-733
19	26	47.3	10	18	US-09-458-298-760
20	26	47.3	10	18	US-09-458-298-1025
21	26	47.3	10	18	US-09-458-298-1267
22	26	47.3	10	18	US-09-458-298-1553
23	26	47.3	10	18	US-09-458-298-1643
24	26	47.3	10	18	US-09-458-298-1905
25	26	47.3	10	18	US-09-458-298A-50
26	26	47.3	10	18	US-09-458-298A-75
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28	26	47.3	10	18	US-09-458-298A-760
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33	26	47.3	10	18	US-09-458-298A-1905
34	26	47.3	10	18	US-09-458-298B-50
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38	26	47.3	10	18	US-09-458-298B-1025
39	26	47.3	10	18	US-09-458-298B-1267
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41	26	47.3	10	18	US-09-458-298B-1643
42	26	47.3	10	18	US-09-458-298B-1905
43	26	47.3	10	26	US-10-005-480A-151
44	26	47.3	10	26	US-10-005-480A-207
45	26	47.3	10	26	US-10-005-480A-421

ALIGNMENTS

RESULT 1
US-10-795-795-6
; Sequence 6, Application US/10795795
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-795-795-6

Query Match 100.0%; Score 55; DB 33; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYFIAAEV 10
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Db 1 WEYFIAAEV 10

RESULT 2

US-10-795-795-5
; Sequence 5, Application US/10795795
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-5

Query Match 60.0%; Score 33; DB 33; Length 10;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYFI 5
| | | | |
Db 6 WEYFI 10

RESULT 3

US-10-937-912-105
; Sequence 105, Application US/10937912
; GENERAL INFORMATION:
; APPLICANT: Baxter International Inc.
; APPLICANT: Johnson, Richard J
; APPLICANT: Maves, Shelley A
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT COMPLEMENT ACTIVATION
; FILE REFERENCE: TR-6067 (BXTR 4017.1)
; CURRENT APPLICATION NUMBER: US/10/937,912
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/501,710
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: complement inhibitor
US-10-937-912-105

Query Match 49.1%; Score 27; DB 35; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYFI 5
| | | | |
Db 6 WEYFI 10

RESULT 4

US-08-347-610-236
; Sequence 236, Application US/08347610
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; NUMBER OF SEQUENCES: 414
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,610
; FILING DATE: 01-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,266
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 014137-005050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 236:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-347-610-236

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
| | | |
Db 7 WQYF 10

RESULT 5

US-08-347-610-237
; Sequence 237, Application US/08347610
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro

APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding Peptides and Their Uses
NUMBER OF SEQUENCES: 414
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,610
FILING DATE: 01-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/159,339
FILING DATE: 29-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,266
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-005050US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 237:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-347-610-237

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 6 WQYF 9

RESULT 6
US-08-347-610-252
; Sequence 252, Application US/08347610
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; NUMBER OF SEQUENCES: 414
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,610
FILING DATE: 01-DEC-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/159,339
FILING DATE: 29-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/186,266
FILING DATE: 25-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 014137-005050US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 252:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-347-610-252

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 2 WQYF 5

RESULT 7
US-08-347-610A-236
; Sequence 236, Application US/08347610A
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; NUMBER OF SEQUENCES: 458
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,266
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Alicea, Hector A.
; REGISTRATION NUMBER: 40,891
; REFERENCE/DOCKET NUMBER: 018623-005050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 236:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-610A-236

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 7 WQYF 10

RESULT 8
US-08-347-610A-237
; Sequence 237, Application US/08347610A
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; NUMBER OF SEQUENCES: 458
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,610A
; FILING DATE: 01-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
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; FILING DATE: 29-NOV-1993
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; APPLICATION NUMBER: US 08/103,396
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; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
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; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,266
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Alicea, Hector A.
; REGISTRATION NUMBER: 40,891
; REFERENCE/DOCKET NUMBER: 018623-005050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 237:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-610A-237

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 6 WQYF 9

RESULT 9
US-08-347-610A-252
; Sequence 252, Application US/08347610A
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; NUMBER OF SEQUENCES: 458
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,610A
; FILING DATE: 01-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,266
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Alicea, Hector A.
; REGISTRATION NUMBER: 40,891
; REFERENCE/DOCKET NUMBER: 018623-005050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-347-610A-252

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 2 WQYF 5

RESULT 10
US-08-347-610B-236
; Sequence 236, Application US/08347610B
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.0050005
; CURRENT APPLICATION NUMBER: US/08/347,610B
; CURRENT FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 236
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigen MAGE
; US-08-347-610B-236

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 7 WQYF 10

RESULT 11
US-08-347-610B-237

; Sequence 237, Application US/08347610B
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.0050005
; CURRENT APPLICATION NUMBER: US/08/347,610B
; CURRENT FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigen MAGE
; US-08-347-610B-237

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 6 WQYF 9

RESULT 12
US-08-347-610B-252
; Sequence 252, Application US/08347610B
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.0050005
; CURRENT APPLICATION NUMBER: US/08/347,610B
; CURRENT FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 252
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigen MAGE
; US-08-347-610B-252

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 2 WQYF 5

RESULT 13
US-08-347-610C-236
; Sequence 236, Application US/08347610C
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.0050005
; CURRENT APPLICATION NUMBER: US/08/347,610C
; CURRENT FILING DATE: 1994-12-10
; PRIOR APPLICATION NUMBER: US 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 236
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigen MAGE
US-08-347-610C-236

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 7 WQYF 10

RESULT 14
US-08-347-610C-237
; Sequence 237, Application US/08347610C
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.0050005
; CURRENT APPLICATION NUMBER: US/08/347,610C
; CURRENT FILING DATE: 1994-12-10
; PRIOR APPLICATION NUMBER: US 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: antigen MAGE
US-08-347-610C-237

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 6 WQYF 9

RESULT 15
US-08-347-610C-252
; Sequence 252, Application US/08347610C
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.0050005
; CURRENT APPLICATION NUMBER: US/08/347,610C
; CURRENT FILING DATE: 1994-12-10
; PRIOR APPLICATION NUMBER: US 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 252
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigen MAGE
US-08-347-610C-252

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 2 WQYF 5

Search completed: September 10, 2005, 01:05:05
Job time : 483 secs

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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:54:57 ; Search time 161 Seconds
(without alignments)
24.499 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WEYFIAAEV 10

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Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 48887

Minimum DB seq length: 10
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	10	US-09-911-129B-6
2	55	100.0	10	16	US-10-795-795-6
3	33	60.0	10	10	US-09-911-129B-5
4	33	60.0	10	16	US-10-795-795-5
5	27	49.1	10	17	US-10-937-912-105
6	26	47.3	10	14	US-10-062-109A-151
7	26	47.3	10	14	US-10-062-109A-207
8	26	47.3	10	14	US-10-062-109A-421
9	26	47.3	10	14	US-10-062-109A-545
10	26	47.3	10	14	US-10-062-109A-637
11	26	47.3	10	14	US-10-005-480A-151

12	26	47.3	10	14	US-10-005-480A-207	Sequence 207, App
13	26	47.3	10	14	US-10-005-480A-421	Sequence 421, App
14	26	47.3	10	14	US-10-005-480A-545	Sequence 545, App
15	26	47.3	10	14	US-10-005-480A-637	Sequence 637, App
16	26	47.3	10	15	US-10-149-135-50	Sequence 50, Appl
17	26	47.3	10	15	US-10-149-135-75	Sequence 75, Appl
18	26	47.3	10	15	US-10-149-135-733	Sequence 733, App
19	26	47.3	10	15	US-10-149-135-760	Sequence 760, App
20	26	47.3	10	15	US-10-149-135-1025	Sequence 1025, Ap
21	26	47.3	10	15	US-10-149-135-1267	Sequence 1267, Ap
22	26	47.3	10	15	US-10-149-135-1553	Sequence 1553, Ap
23	26	47.3	10	15	US-10-149-135-1643	Sequence 1643, Ap
24	26	47.3	10	15	US-10-149-135-1905	Sequence 1905, Ap
25	25	45.5	10	17	US-10-937-794-55	Sequence 55, Appl
26	24	43.6	10	10	US-09-935-384-62	Sequence 62, Appl
27	24	43.6	10	10	US-09-935-384-167	Sequence 167, App
28	24	43.6	10	10	US-09-935-384-168	Sequence 168, App
29	24	43.6	10	10	US-09-935-384-398	Sequence 398, App
30	24	43.6	10	10	US-09-935-384-657	Sequence 657, App
31	24	43.6	10	13	US-10-100-952-162	Sequence 162, App
32	24	43.6	10	13	US-10-100-952-163	Sequence 163, App
33	24	43.6	10	13	US-10-100-952-164	Sequence 164, App
34	24	43.6	10	13	US-10-100-952-165	Sequence 165, App
35	24	43.6	10	14	US-10-005-684-3	Sequence 3, Appli
36	24	43.6	10	14	US-10-005-684-5	Sequence 5, Appli
37	24	43.6	10	14	US-10-347-562-32	Sequence 32, Appl
38	24	43.6	10	14	US-10-347-562-33	Sequence 33, Appl
39	24	43.6	10	14	US-10-347-562-44	Sequence 44, Appl
40	24	43.6	10	14	US-10-347-562-45	Sequence 45, Appl
41	24	43.6	10	14	US-10-351-641-1572	Sequence 1572, Ap
42	24	43.6	10	14	US-10-351-641-1573	Sequence 1573, Ap
43	24	43.6	10	14	US-10-351-641-1584	Sequence 1584, Ap
44	24	43.6	10	14	US-10-351-641-1585	Sequence 1585, Ap
45	24	43.6	10	15	US-10-394-980-402	Sequence 402, App

ALIGNMENTS

RESULT 1
US-09-911-129B-6
; Sequence 6, Application US/09911129B
; Publication No. US20030040600A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-6

Query Match 100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYFIAAEV 10
DB 1 WEYFIAAEV 10

RESULT 2
US-10-795-795-6
; Sequence 6, Application US/10795795
; Publication No. US20040186271A1
; GENERAL INFORMATION:

```
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-6

Query Match      100.0%; Score 55; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFIAAEV 10
        |||||
Db      1 WEYFIAAEV 10

RESULT 3
US-09-911-129B-5
; Sequence 5, Application US/09911129B
; Publication No. US20030040600A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-5

Query Match      60.0%; Score 33; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFI 5
        |||||
Db      6 WEYFI 10

RESULT 4
US-10-795-795-5
; Sequence 5, Application US/10795795
; Publication No. US20040186271A1
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/10/795,795
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/09/911,129B
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-795-795-5

Query Match      60.0%; Score 55; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFIAAEV 10
        |||||
Db      1 WEYFIAAEV 10

RESULT 5
US-10-937-912-105
; Sequence 105, Application US/10937912
; Publication No. US20050090448A1
; GENERAL INFORMATION:
; APPLICANT: Baxter International Inc.
; APPLICANT: Johnson, Richard J
; APPLICANT: Maves, Shelley A
; TITLE OF INVENTION: PEPTIDES THAT INHIBIT COMPLEMENT ACTIVATION
; FILE REFERENCE: TR-6067 (BXR 4017.1)
; CURRENT APPLICATION NUMBER: US/10/937,912
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US 60/501,710
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 105
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: complement inhibitor
US-10-937-912-105

Query Match      49.1%; Score 27; DB 17; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYFI 5
        |||:
Db      6 WEFFL 10

RESULT 6
US-10-062-109A-151
; Sequence 151, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-151
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Query Match 47.3%; Score 26; DB 14; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 3 WDYF 6

RESULT 7

US-10-062-109A-207
; Sequence 207, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-207

Query Match 47.3%; Score 26; DB 14; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 3 WDYF 6

RESULT 8

US-10-062-109A-421
; Sequence 421, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-062-109A-421

Query Match 47.3%; Score 26; DB 14; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 3 WDYF 6

RESULT 9

US-10-062-109A-545
; Sequence 545, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-545

Query Match 47.3%; Score 26; DB 14; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 3 WDYF 6

RESULT 10

US-10-062-109A-637
; Sequence 637, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 637
; LENGTH: 10
; TYPE: PRT

```
; ORGANISM: Homo sapiens
US-10-062-109A-637

Query Match
Best Local Similarity 47.3%; Score 26; DB 14; Length 10;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WDYF 6

RESULT 11
US-10-005-480A-151
; Sequence 151, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-151

Query Match
Best Local Similarity 47.3%; Score 26; DB 14; Length 10;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WDYF 6

RESULT 12
US-10-005-480A-207
; Sequence 207, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-207

Query Match
Best Local Similarity 47.3%; Score 26; DB 14; Length 10;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WDYF 6

RESULT 13
US-10-005-480A-421
; Sequence 421, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-421

Query Match
Best Local Similarity 47.3%; Score 26; DB 14; Length 10;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WDYF 6

RESULT 14
US-10-005-480A-545
; Sequence 545, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-545

Query Match
Best Local Similarity 47.3%; Score 26; DB 14; Length 10;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WDYF 6
```


Qy 1 WEYF 4
|:|
Db 3 WDYF 6

RESULT 15

US-10-005-480A-637
; Sequence 637, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: Cancer
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 785
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 637
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-637

Query Match 47.3%; Score 26; DB 14; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
|:|
Db 3 WDYF 6

Search completed: September 10, 2005, 01:07:52
Job time : 162 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:55:52 ; Search time 74 Seconds
(without alignments)
21.694 Million cell updates/sec

Title: US-10-795-795-6

Perfect score: 55

Sequence: 1 WEYFIAEEV 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 745253 seqs, 160534434 residues

Total number of hits satisfying chosen parameters: 19467

Minimum DB seq length: 10

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New.*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	47.3	10	6	US-10-817-970-4176
2	26	47.3	10	6	US-10-817-970-4177
3	26	47.3	10	6	US-10-817-970-4192
4	26	47.3	10	6	US-10-817-970-4308
5	26	47.3	10	7	US-11-097-912-151
6	26	47.3	10	7	US-11-097-912-207
7	26	47.3	10	7	US-11-097-912-421
8	26	47.3	10	7	US-11-097-912-545
9	26	47.3	10	7	US-11-097-912-637
10	26	47.3	10	7	US-11-097-864-151
11	26	47.3	10	7	US-11-097-864-207
12	26	47.3	10	7	US-11-097-864-421
13	26	47.3	10	7	US-11-097-864-545
14	26	47.3	10	7	US-11-097-864-637
15	24	43.6	10	6	US-10-351-641B-1572
16	24	43.6	10	6	US-10-351-641B-1573
17	24	43.6	10	6	US-10-351-641B-1584
18	24	43.6	10	6	US-10-351-641B-1585
19	24	43.6	10	7	US-11-129-260-1
20	21	38.2	10	6	US-10-817-970-6771
21	21	38.2	10	6	US-10-527-496-41
22	21	38.2	10	6	US-10-492-942-32
23	21	38.2	10	7	US-11-066-697-145
24	21	38.2	10	7	US-11-155-595-3
25	21	38.2	10	7	US-11-178-146-35

Sequence 1, Appli
Sequence 5543, Ap
Sequence 8985, Ap
Sequence 4139, Ap
Sequence 282, Ap
Sequence 10, Appl
Sequence 11, Appl
Sequence 73, Appl
Sequence 296, Ap
Sequence 4640, Ap
Sequence 6743, Ap
Sequence 10072, A
Sequence 57, Appl
Sequence 368, Ap
Sequence 1243, Ap
Sequence 6962, Ap
Sequence 14226, A
Sequence 1046, Ap
Sequence 1214, Ap

21 38.2 10 7 US-11-192-754-1
21 38.2 10 7 US-11-045-024-5543
28 36.4 10 5 US-09-749-280D-8985
29 36.4 10 6 US-10-817-970-4139
30 36.4 10 6 US-10-104-408A-282
31 36.4 10 7 US-11-129-260-11
32 36.4 10 7 US-11-129-260-11
33 36.4 10 7 US-11-097-912-73
34 36.4 10 7 US-11-097-864-73
35 36.4 10 7 US-11-045-024-296
36 36.4 10 7 US-11-045-024-4640
37 36.4 10 7 US-11-045-024-6743
38 36.4 10 7 US-11-045-024-10072
39 36.4 10 7 US-11-199-820-57
40 19 34.5 10 6 US-10-817-970-368
41 19 34.5 10 6 US-10-817-970-1243
42 19 34.5 10 6 US-10-817-970-6962
43 19 34.5 10 6 US-10-817-970-14226
44 19 34.5 10 6 US-10-946-647-1046
45 19 34.5 10 6 US-10-946-647-1214

ALIGNMENTS

RESULT 1

US-10-817-970-4176
; Sequence 4176, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidhey, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, B.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.050000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4176
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4176

Query Match

47.3%; Score 26; DB 6; Length 10;

Best Local Similarity 75.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

QY 1 WEYF 4
|:|
Db 7 WQYF 10

RESULT 2
US-10-817-970-4177
; Sequence 4177, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4177
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4177

Query Match 47.3%; Score 26; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 6 WQYF 9

RESULT 3
US-10-817-970-4192
; Sequence 4192, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.

; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4192
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4192

Query Match 47.3%; Score 26; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
|:|
Db 2 WQYF 5

RESULT 4
US-10-817-970-4308
; Sequence 4308, Application US/10817970
; GENERAL INFORMATION:
; APPLICANT: Grey, H.
; APPLICANT: Sette, A.
; APPLICANT: Sidney, J.
; APPLICANT: Southwood, S.
; APPLICANT: Kubo, R.
; APPLICANT: Celis, E.
; APPLICANT: Chesnut, R.
; APPLICANT: Kast, W.M.
; TITLE OF INVENTION: HLA Binding Motifs and Peptides and Their Uses
; FILE REFERENCE: 2060.0500000
; CURRENT APPLICATION NUMBER: US/10/817,970
; CURRENT FILING DATE: 2004-04-06
; PRIOR APPLICATION NUMBER: 08/821,739
; PRIOR FILING DATE: 1997-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25

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; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 14635
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4308
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-817-970-4308

Query Match          47.3%; Score 26; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 7 WQYF 10

RESULT 5
US-11-097-912-151
; Sequence 151, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-151

Query Match          47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WQYF 6

RESULT 6
US-11-097-912-207
; Sequence 207, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
```

```
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-207

Query Match          47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WQYF 6

RESULT 7
US-11-097-912-421
; Sequence 421, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-421

Query Match          47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WEYF 4
Db 3 WQYF 6

RESULT 8
US-11-097-912-545
; Sequence 545, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
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; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-545

Query Match      47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |:|
Db      3 WDYF 6

RESULT 9
US-11-097-912-637
; SEQUENCE 637, Application US/11097912
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 637
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-637

Query Match      47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |:|
Db      3 WDYF 6

RESULT 10
US-11-097-864-151
; SEQUENCE 151, Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
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; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-151

Query Match      47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |:|
Db      3 WDYF 6

RESULT 11
US-11-097-864-207
; SEQUENCE 207, Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-207

Query Match      47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WEYF 4
        |:|
Db      3 WDYF 6

RESULT 12
US-11-097-864-421
; SEQUENCE 421, Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
```

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-421

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
|:|
Db 3 WDYP 6

RESULT 13
US-11-097-864-545
; Sequence 545 Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 545
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-545

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
|:|
Db 3 WDYP 6

RESULT 14
US-11-097-864-637
; Sequence 637 Application US/11097864
; GENERAL INFORMATION:
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B

; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 637
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-637

Query Match 47.3%; Score 26; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
|:|
Db 3 WDYP 6

RESULT 15
US-10-351-641B-1572
; Sequence 1572 Application US/10351641B
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: DNA ENCODING T-1249 AND OTHER VIRAL FUSION INHIBITOR
; TITLE OF INVENTION: PEPTIDES USEFUL FOR TREATING AIDS
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641B
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1791
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1572
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641B-1572

Query Match 43.6%; Score 24; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WEYF 4
|:|
Db 7 WEWF 10

Search completed: September 10, 2005, 01:09:14
Job time : 75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:29:16 ; Search time 53 Seconds
(without alignments)
96.619 Million cell updates/sec

Title: US-10-795-795-6
Perfect score: 55
Sequence: 1 WEYFIAREV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1093

Minimum DB seq length: 10
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.7	10	1 GON1 ALLMI	P37041 alligator m
2	18	32.7	10	1 GON3 ONCKE	P20367 oncorhynch
3	17	30.9	10	2 Q7M530	Q7M530 pyrococcus
4	17	30.9	10	2 Q93T35	Q93T35 acinetobact
5	16	29.1	10	1 HTF TABAT	P14596 tabanus atr
6	16	29.1	10	2 Q8WT74	Q8WT74 homo sapien
7	16	29.1	10	2 Q9UC04	Q9UC04 homo sapien
8	16	29.1	10	2 Q71UL3	Q71UL3 halictis ru
9	15.5	28.2	10	1 GON1 CHEPR	P80677 chelyosoma
10	15	27.3	10	2 Q7SA62	Q7SA62 neurospora
11	15	27.3	10	2 Q7RS14	Q7RS14 plasmodium
12	15	27.3	10	2 Q70F01	Q70F01 sus scrofa
13	15	27.3	10	2 P96305	P96305 alteromonas
14	15	27.3	10	2 P96306	P96306 aeromonas s
15	15	27.3	10	2 P96321	P96321 escherichia
16	15	27.3	10	2 P96352	P96352 marinobacte
17	15	27.3	10	2 P96421	P96421 neisseria g
18	15	27.3	10	2 Q93LE5	Q93LE5 photobacter
19	15	27.3	10	2 P96423	P96423 pseudomonas
20	15	27.3	10	2 O42355	O42355 brachydanio
21	14	25.5	10	1 TKNK PIG	P67934 sus scrofa
22	14	25.5	10	1 TKNK_RANRI	P67935 rana ridibu
23	14	25.5	10	2 Q9UC08	Q9UC08 homo sapien
24	14	25.5	10	2 Q94VD2	Q94VD2 varanus pan
25	14	25.5	10	2 Q52762	Q52762 rhizobium s
26	14	25.5	10	2 Q6JL97	Q6JL97 neisseria g
27	14	25.5	10	2 Q9AE19	Q9AE19 streptococc
28	14	25.5	10	2 Q9QV21	Q9QV21 rattus sp.
29	14	25.5	10	2 Q83978	Q83978 influenza a
30	13	23.6	10	1 CATB SHEEP	P83205 ovis aries
31	13	23.6	10	1 GAJU_HUMAN	P01358 homo sapien

32	13	23.6	10	1 GON1 CLUPA	P81749 clupea pall
33	13	23.6	10	1 GON2 ALLMI	P68073 alligator m
34	13	23.6	10	1 GON2 CHICK	P68072 gallus gall
35	13	23.6	10	1 GON2 CLUPA	P68075 clupea pall
36	13	23.6	10	1 GON2 HYDCO	P68076 hydrolagus
37	13	23.6	10	1 GON2 SQUAC	P68074 squalus aca
38	13	23.6	10	1 GON3 PETMA	P30948 petromyzon
39	13	23.6	10	1 GON1 SQUAC	P27429 squalus aca
40	13	23.6	10	1 MDR2 SOYBN	Q58976 glycine max
41	13	23.6	10	1 NO40 TOBAC	P55962 nicotiana t
42	13	23.6	10	1 Q2OG COMTE	P80466 comamonas t
43	13	23.6	10	2 Q69FE6	Q69FE6 phomopsis s
44	13	23.6	10	2 Q69FE7	Q69FE7 phomopsis s
45	13	23.6	10	2 Q7MAX7	Q7MAX7 fusarium sp

ALIGNMENTS

RESULT 1

GON1 ALLMI

ID GON1 ALLMI STANDARD; PRT; 10 AA.

AC P37041; P20407;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH I)

DE (Luliberin I).

OS Alligator mississippiensis (American alligator).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Crocodylidae; Alligatorinae; Alligator.

OX NCBI_TaxID=8496;

RN [1]

RP SEQUENCE.

TX TISSUE=Brain;

RC MEDLINE=91352338; PubMed=1882082; DOI=10.1016/0167-0115(91)90206-V;

RA Lovejoy D.A., Fischer W.H., Parker D.B., Mccrory J.E., Park M.,

RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;

RT "Primary structure of two forms of gonadotropin-releasing hormone from

RT brains of the American alligator (Alligator mississippiensis).";

RL Regul. Pept. 33:105-116(1991).

CC -I- FUNCTION: Stimulates the secretion of gonadotropins.

CC -I- SUBCELLULAR LOCATION: Secreted.

CC -I- SIMILARITY: Belongs to the GnRH family.

DR PIR; A60066; RHAQ1.

DR InterPro; IPR002012; GnRH.

DR Pfam; PF00446; GnRH; 1.

DR PROSITE; PS00473; GnRH; 1.

KW Amidation; Direct protein sequencing; Hormone; Hypothalamus;

KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 Pyrrolidone carboxylic acid.

FT MOD_RES 10 10 Glycine amide.

SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 32.7%; Score 18; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 2e+04;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3

DB 3 WSY 5

RESULT 2

GON3 ONCKE

ID GON3 ONCKE STANDARD; PRT; 10 AA.

AC P20367; P81751;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-

DE RH III) (Luliberin III).

GN Name=GNRH3;

OS Oncorhynchus keta (Chum salmon), and
 OS Clupea pallasii (Pacific herring).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8018, 30724;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=O.keta;
 RX MEDLINE=83195140; PubMed=6341999;
 RA Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
 RT "Characterization of a teleost gonadotropin-releasing hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
 RN [2]
 RP SEQUENCE, AND FUNCTION.
 RC SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
 RX MEDLINE=20114351; PubMed=10650929; DOI=10.1210/en.141.2.505;
 RA Carolefeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
 RA Chang J.P., Rivier J.E., Sherwood N.M.;
 RT "Primary structure and function of three gonadotropin-releasing
 RT hormones, including a novel form, from an ancient teleost, herring.";
 RL Endocrinology 141:505-512(2000).
 CC -I- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the GnRH family.
 DR PIR; A21114;
 DR InterPro; IPR002012; GnRH.
 DR Pfam; PF00446; GnRH; 1.
 DR PROSITE; PS00473; GnRH; 1.
 KW Amidation; Direct protein sequencing; Hormone; Hypothalamus;
 KW Pyrrolidone carboxylic acid.
 FT MOD RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD RES 10 10 Glycine amide.
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1230 MW; 284B3233786B45A3 CRC64;
 Query Match 32.7%; Score 18; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 2e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WEY 3
 Db | | |
 3 WSY 5
 RESULT 3
 ID Q7M530 PRELIMINARY; PRT; 10 AA.
 AC Q7M530;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Aldehyde ferredoxin oxidoreductase (EC 1.2.7.-) (Fragment).
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91317766; PubMed=1907273;
 RA Mukund S.; Adams M.W.W.;
 RT "The novel tungsten-iron-sulfur protein of the hyperthermophilic
 RT archaeobacterium, Pyrococcus furiosus, is an aldehyde ferredoxin
 RT oxidoreductase. Evidence for its participation in a unique glycolytic
 RT pathway.";
 RL J. Biol. Chem. 266:14208-14216(1991).
 DR PIR; A40753; A40753.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1272 MW; 3E3260D408637448 CRC64;
 Query Match 30.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WEY 3
 Db | | |
 3 WSY 5
 RESULT 3
 ID Q7M530 PRELIMINARY; PRT; 10 AA.
 AC Q7M530;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Aldehyde ferredoxin oxidoreductase (EC 1.2.7.-) (Fragment).
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91317766; PubMed=1907273;
 RA Mukund S.; Adams M.W.W.;
 RT "The novel tungsten-iron-sulfur protein of the hyperthermophilic
 RT archaeobacterium, Pyrococcus furiosus, is an aldehyde ferredoxin
 RT oxidoreductase. Evidence for its participation in a unique glycolytic
 RT pathway.";
 RL J. Biol. Chem. 266:14208-14216(1991).
 DR PIR; A40753; A40753.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1272 MW; 3E3260D408637448 CRC64;
 Query Match 30.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 WEY 3
 Db | | |
 3 WSY 5

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WEYFI 5
 Db | | |
 5 WGRFI 9
 RESULT 4
 ID Q93T35 PRELIMINARY; PRT; 10 AA.
 AC Q93T35;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Quaternary ammonium compound-resistance protein (Fragment).
 GN Name=qaqEdelta1;
 OS Acinetobacter genomosp. 3.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OX NCBI_TaxID=48296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YMCU160;
 RX MEDLINE=21999242; PubMed=12003980;
 RA Yum J.H., Yi K., Lee H., Yong D., Lee K., Kim J.M., Rossolini G.M.,
 RA Chong Y.;
 RT "Molecular characterization of metallo-b-lactamase-producing
 RT Acinetobacter baumannii and Acinetobacter genomosp. 3 from Korea:
 RT identification of two new integrons carrying the bla(VIM-2) gene
 RT cassettes.";
 RL J. Antimicrob. Chemother. 49:837-840(2002).
 DR ENBL; AF369871; AAK54205.1; -.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1178 MW; 2E287BC729C73378 CRC64;
 Query Match 30.9%; Score 17; DB 2; Length 10;
 Best Local Similarity 28.6%; Pred. No. 3.1e+04;
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 WEYFIAA 7
 Db | | |
 4 WLFLVIA 10
 RESULT 5
 ID HTF TABAT STANDARD; PRT; 10 AA.
 AC PI4596;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
 DE (DCC II).
 OS Tabanus atratus (Horse fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
 OC Tabanus.
 OX NCBI_TaxID=7207;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90046758; PubMed=2813385;
 RA Jaffe H., Raina A.K., Riley C.I., Fraser B.A., Nachman R.J.,
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
 RT "Primary structure of two neuropeptide hormones with adipokinetic and
 RT hypotrehalosaemic activity isolated from the corpora cardiaca of horse
 RT flies (Diptera).";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
 CC -I- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
 CC elevate the level of trehalose in the hemolymph of insects).
 CC major carbohydrate in the hemolymph of insects).
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.

```
DR PIR; B33995; B33995.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Amidation; Direct protein sequencing; Neuropeptide;  
KW Pyroglutamate carboxylic acid.  
FT MOD_RES 1 1 Pyroglutamate carboxylic acid.  
FT MOD_RES 10 10 Tyrosine amide.  
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;  
  
Query Match 29.1%; Score 16; DB 1; Length 10;  
Best Local Similarity 66.7%; Pred. No. 4.8e+04;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 WEY 3  
DB 8 WGY 10  
  
RESULT 6  
Q8WTT4  
ID Q8WTT4 PRELIMINARY; PRT; 10 AA.  
AC Q8WTT4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Dystrophin (Fragment).  
GN Names=dystrophin; Synonyms=DMD;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Ditta S.D., Klamut H.J., Ray P.N., Worton R.G.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Beggs A.H., Koenig M., Kunkel L.M.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA den Dunnen J.T.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF276053; AAL35752.1; -.  
DR EMBL; AF213401; AAL61549.1; -.  
FT NON_TER 10 10  
SQ SEQUENCE 10 AA; 1340 MW; 2B999202CB1B0363 CRC64;  
  
Query Match 29.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.8e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WE 2  
DB 4 WE 5  
  
RESULT 7  
Q9UCQ4  
ID Q9UCQ4 PRELIMINARY; PRT; 10 AA.  
AC Q9UCQ4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE P42=42 kDa NON-muscle cytoplasmic actin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=92162059; PubMed=1789797;  
RA Miyamoto S., Wu J.M.;
```

```
RT Identification of a 38-kDa protein (p38) in HL-60 leukemic cells as a  
RT truncated actin.;  
RL Biochem. Int. 25:307-319(1991).  
DR GO; GO:0015629; C:actin cytoskeleton; NAS.  
DR GO; GO:0003774; F:motor activity; NAS.  
FT NON_TER 1 1  
FT NON_TER 10 10  
SQ SEQUENCE 10 AA; 1146 MW; DB131DEB1B076DC2 CRC64;  
  
Query Match 29.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.8e+04;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5 IAAEE 9  
DB 3 VAPEE 7  
  
RESULT 8  
Q71UL3  
ID Q71UL3 PRELIMINARY; PRT; 10 AA.  
AC Q71UL3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Lysin (Fragment).  
OS Haliotis rufescens (California red abalone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Vetigastropoda; Haliotidae; Haliotis.  
OX NCBI_TaxID=6454;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98393704; PubMed=9724763; DOI=10.1073/pnas.95.18.10676;  
RA Metz E.C., Robles-Sikisaka R., Vacquier V.D.;  
RT "Nonsynonymous substitution in abalone sperm fertilization genes  
RT exceeds substitution in introns and mitochondrial DNA.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:10676-10681(1998).  
DR EMBL; AF076820; AAC35348.1; -.  
FT NON_TER 1 1  
FT NON_TER 10 10  
SQ SEQUENCE 10 AA; 1196 MW; C507DF572DD33326 CRC64;  
  
Query Match 29.1%; Score 16; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 4.8e+04;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 YFI 5  
DB 8 YFV 10  
  
RESULT 9  
GON1_CHEPR  
ID GON1_CHEPR STANDARD; PRT; 10 AA.  
AC P80677;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (Luliberin  
DE 1).  
OS Chelyosoma productum.  
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
OC Phlebobranchia; Corellidae; Chelyosoma.  
OX NCBI_TaxID=71177;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RX MEDLINE=96413669; PubMed=8816823; DOI=10.1073/pnas.93.19.10461;  
RA Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,  
RA Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;  
RT "Two new forms of gonadotropin-releasing hormone in a protochordate  
RT and the evolutionary implications";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).  
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
```

CC		the secretion of both luteinizing and follicle-stimulating hormones.
CC	-!	SUBCELLULAR LOCATION: Secreted.
CC	-!	TISSUE SPECIFICITY: GnRH neurons lie within blood sinuses close to the gonaducts and gonads in both juveniles and adults, implying that the neuropeptide is released into the bloodstream.
CC	-!	MASS SPECTROMETRY: MW=1246.56; METHOD=WALDI; RANGE=1-10; NOTE=Ref.1.
CC	-!	SIMILARITY: Belongs to the GnRH family.
DR	InterPro:	IPR002012; GnRH.
DR	Pfam:	PF00446; GnRH; 1.
DR	PROSITE:	PS00473; GnRH; 1.
KW	Annotation:	Direct protein sequencing; Hormone;
DW	Pyroglutamate:	Pyroglutamate carboxylic acid.
FT	MOD_RES	1 1 Pyroglutamate carboxylic acid.
FT	MOD_RES	10 10 Glycine amide (By similarity).
FT	SEQUENCE	10 AA; 1264 MW; 284B3639DB5AB5A3 CRC64;
QY	Query Match	28.2%; Score 15.5; DB 1; Length 10;
DB	Best Local Similarity	60.0%; Pred. No. 6e+04;
	Matches	3; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY	1 W-BYP 4	
	:	
DB	3 WSDYF 7	
RESULT 10		
ID Q7SA62	PRELIMINARY;	PRT; 10 AA.
AC AC	O7SA62;	
DT DT	01-MAR-2004 (T-EMBLrel. 26, Created)	
DT DT	01-MAR-2004 (T-EMBLrel. 26, Last sequence update)	
DT DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)	
DE DE	Predicted protein.	
GN GN	Names=NCU08327.1;	
OS OS	Neurospora crassa.	
OC OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
OC OC	Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.	
OX OX	NCBI_TaxID=5141;	
RN RN	[1]	
RP RP	SEQUENCE FROM N.A.	
RC RC	STRAIN=OR74A;	
RA RA	Galagan J.E.; Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,	
RA RA	Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,	
RA RA	Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,	
RA RA	Qui D., Iankiev P., Petersen D., Nelson M., Washburne M.,	
RA RA	Selitretnikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,	
RA RA	Kothe G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,	
RA RA	Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,	
RA RA	Kamal M., Kamysellis M., Maucelli E., Bielke C., Rudd S., Frishman D.,	
RA RA	Krystofova S., Rasmussen C., Metzgerberg R.L., Perkins D.D., Kroken S.,	
RA RA	Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,	
RA RA	DaSouza C.C., Glass L., Orbach M.J., Berglund J., Voslaker R.,	
RA RA	Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,	
RA RA	Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freilich M.,	
RA RA	Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.	
RL RL	"The Genome Sequence of the Filamentous Fungus Neurospora crassa.";	
RT RT	Nature 0:0-0(2003).	
CC -!	CAUTION: The sequence shown here is derived from an	
CC CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.	
CC CC	EMBL: AABX01000206; EAA33304.1; "	
SO SO	SEQUENCE 10 AA; 1284 MW; D6D34CB72DC40059 CRC64;	

Query Match	27.3%	Score 15;	DB 2;	Length 10;
Best Local Similarity	60.0%	Prsa No. 7.5e+04;		
Matches	3;	Conservative 1;	Mismatches 1;	Indels 0;
Gaps	0;			

RESULT 11	
QID	Q7RSI4
ID	PRELIMINARY; PRT; 10 AA.
AC	O7RSI4;
DT	01-MAR-2004 (TrEMBLrel. 26, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein.
GN	Name=PY00373;
OS	Plasmodium yoelii yoelii.
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX	NCBI_Taxid=73239;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=17XNL;
RX	PubMed=12368865; DOI=10.1038/nature01099;
RA	Carlton J.M., Angiuoli S.V., Suh B.B., Koijg T.W., Perteza M.,
RA	Salva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA	Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA	Shallon S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA	Cho J.K., Quackenbush J.J., Sedegah M., Shoabi A., Cummings L.M.,
RA	Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA	Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA	van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA	Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA	Carucci D.J.;
RT	Genome sequence and comparative analysis of the model rodent malaria
RT	parasite Plasmodium yoelii yoelii.";
RL	Nature 419:512-519(2002).
CC	-!- CAUTION: The sequence shown here is derived from an
CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC	preliminary data.
CC	EWBL: AABL01000104; EAA15335.1; -.
DR	Hypothetical protein.
KW	SEQUENCE 10 AA; 1279 MW; 11EBECB04B4B4B50 CRC64;
SK	
Query Match 27.3%; Score 15; DB 2; Length 10;	
Best Local Similarity 50.0%; Pred. No. 7.5e+04;	
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

Qy	3 YFTA 6 : :
Dd	5 YYIS 8
RESULT 12	
Q70F01	PRELIMINARY; PRT; 10 AA.
ID Q70F01	
AC Q70F01;	2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004	(TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE DE	Calpastatin type 2 (Fragment) .
GN Name=CAST;	
OS Sw scrofa (Pig) .	
OC Eukaryota; Metazoa;	Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria;	Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_taxid=9823;	
[1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=21531263;	PubMed=11673859; DOI=10.1006/abbi.2001.2546;
RA Parr T.; Sensky P.L., Bardsley R.G., Buttery P.J.;	
RT "Calpastatin expression in porcine cardiac and skeletal muscle and	
RT partial gene structure."	
RL Arch. Biochem. Biophys. 395:1-13(2001).	
RN [2]	
RP SEQUENCE FROM N.A.	
RA Parr T.;	
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AJ583410; CAE47431.1; -.	
FT NON TER 10	
SO SEQUENCE 10 AA; 1291 MW; CFF912436365BDD9 CRC64;	

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.5e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WEY 3
| | |
DB 6 WWY 8

RESULT 13
P96305 PRELIMINARY; PRT; 10 AA.
AC P96305;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Alteromonas haloplanktis (Pseudoalteromonas haloplanktis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Pseudoalteromonadaceae; Pseudoalteromonas.
OX NCBI_TaxID=228;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14393;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68076; AAB48021.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1053 MW; 857BD235AB544AAA CRC64;

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFTAA 7
| | |
DB 6 YSLAA 10

RESULT 14
P96306 PRELIMINARY; PRT; 10 AA.
AC P96306;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33658;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
DR EMBL; U68075; AAB48022.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFTAA 7
| | |
DB 6 YALAA 10

RESULT 15
P96321

ID P96321 PRELIMINARY; PRT; 10 AA.
AC P96321;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Coded portion of proteolysis tag (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=97128184; PubMed=8972778;
RA Williams K.P., Bartel D.P.;
RT "Phylogenetic analysis of tmRNA secondary structure."
RL RNA 2:1306-1310(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 133;
RX MEDLINE=95023883; PubMed=7524073;
RA Komine Y., Kitabatake M., Yokogawa T., Nishikawa K., Inokuchi H.;
RT "A tRNA-like structure is present in 10Sa RNA, a small stable RNA from
RT Escherichia coli."
RL Proc. Natl. Acad. Sci. U.S.A. 91:9223-9227(1994).
DR EMBL; U68074; AAB48024.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1051 MW; 857BD22DCB544B1A CRC64;

Query Match 27.3%; Score 15; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YFTAA 7
| | |
DB 6 YALAA 10

Search completed: September 10, 2005, 00:55:48
Job time : 55 secs

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OM protein - protein search, using sw model

Run on: September 10, 2005, 01:12:15 ; Search time 74 Seconds
(without alignments)
10.847 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 745253 seqs, 160534434 residues

Total number of hits satisfying chosen parameters: 5221

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pcp.*
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3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pcp.*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pcp.*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pcp.*
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8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	73.1	5	7	US-11-004-399-2954
2	16	61.5	5	7	US-11-004-399-1768
3	15	57.7	5	6	US-10-536-067-13
4	15	57.7	5	6	US-10-395-607A-197
5	14	53.8	5	7	US-11-004-399-1254
6	14	53.8	5	7	US-11-030-300-22
7	13	50.0	5	1	PCT-US04-39427-19
8	13	50.0	5	1	PCT-US04-39427-21
9	13	50.0	5	5	US-09-424-840-54
10	13	50.0	5	5	US-09-700-179B-69
11	13	50.0	5	5	US-09-424-840-54
12	13	50.0	5	5	US-09-920-306B-43
13	13	50.0	5	5	US-09-071-838A-116
14	13	50.0	5	6	US-10-953-116-16
15	13	50.0	5	6	US-10-953-119-21
16	13	50.0	5	6	US-10-953-110A-17
17	13	50.0	5	6	US-10-953-116A-16
18	13	50.0	5	6	US-10-953-119A-21
19	13	50.0	5	6	US-10-953-110B-17
20	13	50.0	5	6	US-10-997-759-19
21	13	50.0	5	6	US-10-997-759-21
22	13	50.0	5	7	US-11-004-399-1649
23	13	50.0	5	7	US-11-004-399-2093
24	13	50.0	5	7	US-11-129-741-1017
25	13	50.0	5	7	US-11-129-741-4015

Sequence 13, Appl
Sequence 43, Appl
Sequence 62, Appl
Sequence 63, Appl
Sequence 18, Appl
Sequence 20, Appl
Sequence 36, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 40, Appl
Sequence 39, Appl
Sequence 8, Appl
Sequence 24, Appl
Sequence 28, Appl
Sequence 1, Appl
Sequence 101, Appl
Sequence 43, Appl
Sequence 62, Appl
Sequence 63, Appl
Sequence 33, Appl

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PCT-US04-35749-63
PCT-US04-39427-18
PCT-US04-39427-20
US-09-601-644B-36
US-09-920-306B-38
US-09-920-306B-39
US-09-920-306B-40
US-09-954-737C-39
US-09-251-638C-8
US-10-876-343A-24
US-10-876-343A-28
US-10-496-869-1
US-10-980-989A-101
US-10-975-157-43
US-10-975-157-62
US-10-975-157-63
US-10-156-820A-33

ALIGNMENTS

RESULT 1

US-11-004-399-2954
Sequence 2954, Application US/11004399
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
APPLICANT: Peiris, Joseph Sriyal Malik
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
FILE REFERENCE: 2587/73166/RDK
CURRENT APPLICATION NUMBER: US/11/004,399
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637
PRIOR FILING DATE: 2003-12-03
NUMBER OF SEQ ID NOS: 4043
SOFTWARE: Patentin version 3.1
SEQ ID NO 2954
LENGTH: 5
TYPE: PRT
ORGANISM: SARS-CoV Virus
US-11-004-399-2954

Query Match 73.1%; Score 19; DB 7; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
DB 2 DNFA 5

RESULT 2

US-11-004-399-1768
Sequence 1768, Application US/11004399
GENERAL INFORMATION:
APPLICANT: Chye, Mee Lee
APPLICANT: Li, Hong Ye
APPLICANT: Ramalingam, Sathiskumar
APPLICANT: Poon, Leo Lit Man
APPLICANT: Peiris, Joseph Sriyal Malik
TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
FILE REFERENCE: 2587/73166/RDK
CURRENT APPLICATION NUMBER: US/11/004,399
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,637

As per previous date

; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1768
; LENGTH: 5
; TYPE: PRT
; ORGANISM: SARS-Cov Virus
US-11-004-399-1768

Query Match 61.5%; Score 16; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NFS 5
Db 1 NFS 3

RESULT 3
US-10-536-067-13

; Sequence 13, Application US/10536067
; GENERAL INFORMATION:
; APPLICANT: Biogen Idec MA Inc.
; APPLICANT: DE FOUGEROLLES, Antonin R.
; APPLICANT: KOTELIANSKI, Victor E.
; APPLICANT: GABER, Ellen
; APPLICANT: REID, Carl
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST MONOCYTE
; TITLE OF INVENTION: CHEMOTACTIC PROTEINS
; FILE REFERENCE: BGN-010PC
; CURRENT APPLICATION NUMBER: US/10/536,067
; PRIOR FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: 60/430007
; PRIOR FILING DATE: 2002-11-27
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-536-067-13

Query Match 57.7%; Score 15; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNF 4
Db 1 DNY 3

RESULT 4
US-10-395-607A-197

; Sequence 197, Application US/10395607A
; GENERAL INFORMATION:
; APPLICANT: Wright, David A.
; APPLICANT: Voytas, Daniel F.
; TITLE OF INVENTION: Plant Retroelements and Methods Related
; TITLE OF INVENTION: Thereto
; FILE REFERENCE: 08411/036001
; CURRENT APPLICATION NUMBER: US/10/395,607A
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 09/586,106
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 09/322,478
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 60/087,125
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 335
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 197

; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus
US-10-395-607A-197

Query Match 57.7%; Score 15; DB 6; Length 5;
Best Local Similarity 50.0%; Pred. No. 6.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDNF 4
Db 2 MDDF 5

RESULT 5

US-11-004-399-1254

; Sequence 1254, Application US/11004399
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-Cov Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against S.
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1254
; LENGTH: 5
; TYPE: PRT
; ORGANISM: SARS-Cov Virus
US-11-004-399-1254

Query Match 53.8%; Score 14; DB 7; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DNFS 5
Db 1 DNFS 4

RESULT 6

US-11-030-300-22

; Sequence 22, Application US/11030300
; GENERAL INFORMATION:
; APPLICANT: ORSER, CINDY S.
; APPLICANT: PAN, TAO
; TITLE OF INVENTION: IMMOBILIZED PROBES AND METHODS OF DETECTING
; TITLE OF INVENTION: CONFORMATIONALLY ALTERED PRION PROTEINS
; FILE REFERENCE: ADL-102
; CURRENT APPLICATION NUMBER: US/11/030,300
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/608,541
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 22
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-030-300-22

Query Match 53.8%; Score 14; DB 7; Length 5;
Best Local Similarity 75.0%; Pred. No. 6.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNF 4
|||
Db 1 LANF 4

RESULT 7
PCT-US04-39427-19
; Sequence 19, Application PC/TUS0439427
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S.
; APPLICANT: Kumaresan, Pappanaicken
; APPLICANT: DeNardo, Sally
; APPLICANT: DeNardo, Gerald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: On-Demand Cleavable Linkers for Radioconjugates for
; TITLE OF INVENTION: Cancer Imaging and Therapy
; FILE REFERENCE: 02307W-140610PC
; CURRENT APPLICATION NUMBER: PCT/US04/39427
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 60/525,236
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pentapeptide
; OTHER INFORMATION: tissue-type plasminogen activator (t-PA) substrate
PCT-US04-39427-19

Query Match 50.0%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
|||
Db 3 DSF 5

RESULT 8
PCT-US04-39427-21
; Sequence 21, Application PC/TUS0439427
; GENERAL INFORMATION:
; APPLICANT: Lam, Kit S.
; APPLICANT: Kumaresan, Pappanaicken
; APPLICANT: DeNardo, Sally
; APPLICANT: DeNardo, Gerald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: On-Demand Cleavable Linkers for Radioconjugates for
; TITLE OF INVENTION: Cancer Imaging and Therapy
; FILE REFERENCE: 02307W-140610PC
; CURRENT APPLICATION NUMBER: PCT/US04/39427
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 60/525,236
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pentapeptide
; OTHER INFORMATION: tissue-type plasminogen activator (t-PA) substrate
PCT-US04-39427-21

Query Match 50.0%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
|||
Db 3 NNF 5

RESULT 9
US-09-424-840-54
; Sequence 54, Application US/09424840
; GENERAL INFORMATION:
; APPLICANT: BERCHTOLD, Peter
; APPLICANT: ESCHER, Robert F.A.
; TITLE OF INVENTION: Anti-Grp94/Grp78 Recombinant Antibodies
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840-54

Query Match 50.0%; Score 13; DB 5; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
|||
Db 1 NFA 3

RESULT 10
US-09-700-1798-69
; Sequence 69, Application US/097001798
; GENERAL INFORMATION:
; APPLICANT: MASCI, PANTALEONE PAUL
; APPLICANT: LAVIN, MARTIN FRANCIS
; APPLICANT: GAFFNEY, PATRICK JOSEPH
; APPLICANT: SOROKINA, NATALYA IGOREVNA
; APPLICANT: FILIPPOVICH, IGOR VLADIMIROVICH
; TITLE OF INVENTION: PLASMIN INHIBITORS FROM THE AUSTRALIAN BROWN SNAKE
; TITLE OF INVENTION: PSEUDONAJA TEXTILIS TEXTILIS
; FILE REFERENCE: 017227-0193
; CURRENT APPLICATION NUMBER: US/09/700,1798
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: PCT/AU99/00343
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: AU PP3450
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 69
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-700-1798-69

Query Match 50.0%; Score 13; DB 5; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
|||
Db 3 NNF 5

```
RESULT 11
US-09-424-840-54
; Sequence 54, Application US/09424840
; GENERAL INFORMATION:
; APPLICANT: BERTCHOLD, Peter
; TITLE OF INVENTION: Anti-GPIIb/IIIa Recombinant Antibodies
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 54
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840-54

Query Match      50.0%; Score 13; DB 5; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 NFS 5
Db      1 NFA 3

RESULT 12
US-09-920-306B-43
; Sequence 43, Application US/09920306B
; GENERAL INFORMATION:
; APPLICANT: Badley, Robert
; APPLICANT: Berry, Mark
; APPLICANT: Williams, Samantha
; TITLE OF INVENTION: Peptides Capable of Functioning as Mimotopes for Hormonal
; FILE REFERENCE: IMIN.P-034
; CURRENT APPLICATION NUMBER: US/09/920,306B
; CURRENT FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 43
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; OTHER INFORMATION: synthetic peptide
US-09-920-306B-43

Query Match      50.0%; Score 13; DB 5; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DNF 4
Db      1 DDF 3

RESULT 13
US-09-071-838A-116
; Sequence 116, Application US/09071838A
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
```

```
;
; Yadegari, Ramin
; Margossian, Linda
; Harada, John
; Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/071,838A
; APPLICATION NUMBER: US/09/071,838A
; FILING DATE: 01-May-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-09-071-838A-116

Query Match      50.0%; Score 13; DB 5; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DNF 4
Db      2 DHF 4

RESULT 14
US-10-953-116-16
; Sequence 16, Application US/10953116
; GENERAL INFORMATION:
; APPLICANT: MICKLE, Travis
; APPLICANT: KRISHNAN, Suma
; APPLICANT: LAUDERBACK, Christopher
; APPLICANT: MILLER, Christal
; APPLICANT: MONCRIEF, James Scott
; APPLICANT: PICCARIELLO, Thomas
; TITLE OF INVENTION: Abuse Resistant Hydrocodone Compounds
; FILE REFERENCE: 54719.000151
; CURRENT APPLICATION NUMBER: US/10/953,116
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/358,368
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/362,082
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/366,258
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/507,012
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/567,800
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/568,011
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; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 10/156,527
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: PCT/US03/05525
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 10/927,257
; PRIOR FILING DATE: 2004-08-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic carrier
US-10-953-116-16

Query Match 50.0%; Score 13; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
|:|
Db 1 DDF 3

RESULT 15
US-10-953-119-21
; Sequence 21, Application US/10953119
; GENERAL INFORMATION:
; APPLICANT: MICKLE, Travis
; APPLICANT: KRISHNAN, Suma
; APPLICANT: MONCRIEF, James Scott
; APPLICANT: LAUDERBACK, Christopher
; APPLICANT: MILLER, Christal
; TITLE OF INVENTION: Pharmaceutical Compositions for Prevention of Overdose
; FILE REFERENCE: 54719.000107
; CURRENT APPLICATION NUMBER: US/10/953,119
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: 60/507,012
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/567,800
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/567,802
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/568,011
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic carrier
US-10-953-119-21

Query Match 50.0%; Score 13; DB 6; Length 5;
Best Local Similarity 66.7%; Pred. No. 6.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNF 4
|:|
Db 1 DDF 3

Search completed: September 10, 2005, 01:25:57
Job time : 75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 01:05:19 ; Search time 38 Seconds
(without alignments)
12.660 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LDNFS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 120

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	13	50.0	5	2 PT0281	Ig heavy chain CRD
2	10	38.5	5	2 PT0624	T-cell receptor be
3	10	38.5	5	4 A58728	serrawettin W2 - S
4	9	34.6	5	2 B31836	20K protein - Rick
5	8	30.8	5	2 A32516	cholecystokinin-5
6	8	30.8	5	2 S70615	endo-1,4-beta-xyla
7	8	30.8	5	2 PT0644	T-cell receptor be
8	7	26.9	5	2 D60274	major protein anti
9	7	26.9	5	2 PT0679	T-cell receptor be
10	7	26.9	5	2 A44892	fulicin - giant AF
11	7	26.9	5	2 PT0600	T-cell receptor be
12	7	26.9	5	2 PT0601	T-cell receptor be
13	7	26.9	5	2 A26830	mitosis inhibiting
14	6	23.1	5	2 A44955	alkanal monooxygen
15	6	23.1	5	2 B60274	major protein anti
16	6	23.1	5	2 PQ0689	photosystem I 10.4
17	6	23.1	5	2 S51077	alpha-amylase - ri
18	6	23.1	5	2 PS0324	ribulose-bisphosph
19	6	23.1	5	2 B45525	actin I - malaria
20	6	23.1	5	2 A37114	hypoxanthine phosph
21	6	23.1	5	2 B61445	Leu-enkephalin - b
22	6	23.1	5	2 A61445	Met-enkephalin - b
23	6	23.1	5	2 B61168	cocoonase (EC 3.4.
24	6	23.1	5	2 JH0253	gut pentapeptide -
25	6	23.1	5	2 PT0267	Ig heavy chain CRD
26	6	23.1	5	2 PT0278	Ig heavy chain CRD
27	6	23.1	5	2 PT0295	Ig heavy chain CRD
28	6	23.1	5	2 PT0308	Ig heavy chain CRD
29	6	23.1	5	2 S62883	seminal plasma pro

30 6 23.1 5 2 PT0596 T-cell receptor be
31 6 23.1 5 2 PT0513 T-cell receptor be
32 6 23.1 5 2 PT0729 T-cell receptor be
33 6 23.1 5 2 PT0672 T-cell receptor be
34 6 23.1 5 2 PT0660 T-cell receptor be
35 6 23.1 5 2 PT0651 T-cell receptor be
36 6 23.1 5 2 PT0656 T-cell receptor be
37 6 23.1 5 2 PT0535 T-cell receptor be
38 6 23.1 5 2 PT0699 T-cell receptor be
39 6 23.1 5 2 PT0561 T-cell receptor be
40 6 23.1 5 2 PT0695 T-cell receptor be
41 6 23.1 5 2 PT0703 T-cell receptor be
42 6 23.1 5 2 PT0690 T-cell receptor be
43 6 23.1 5 2 PT0573 T-cell receptor be
44 6 23.1 5 2 PT0580 T-cell receptor be
45 6 23.1 5 2 S68326 blood cell protein

ALIGNMENTS

RESULT 1

PT0281
IG heavy chain CRD3 region (clone 4-91C) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0281

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0281

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotrimer; immunoglobulin

Query Match 50.0%; Score 13; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5

DB 2 ENWS 5

RESULT 2

PT0624

T-cell receptor beta chain V-D-J region (120-1K) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0624

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0624

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 38.5%; Score 10; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LD 2

DB 4 LD 5

RESULT 3

A58728
 Serawettin W2 - Serratia marcescens
 C;Species: Serratia marcescens
 C;Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
 C;Accession: A58728
 R;Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
 J. Bacteriol. 174, 1769-1776, 1992
 A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and
 A;Reference number: A58728; MUID:92193260; PMID:1548227
 A;Accession: A58728
 A;Status: unencoded polypeptide
 A;Molecule type: protein
 A;Residues: 1-5 <MAT>
 A;Experimental source: strain NS 25
 C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation
 C;Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded
 F;1/Modified site: D-leucine (Ileu) #status experimental
 F;4/Modified site: D-phenylalanine (Phe) #status experimental
 F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status experimental

Query Match 38.5%; Score 10; DB 4; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDNF 4
 | |
 Db 1 LSTF 4

RESULT 4
 B31836
 20K protein - Rickettsia rickettsii (fragment)
 C;Species: Rickettsia rickettsii
 C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
 C;Accession: B31836
 R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
 J. Bacteriol. 170, 4493-4500, 1988
 A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rick
 A;Reference number: A91885; MUID:89008059; PMID:3133629
 A;Accession: B31836
 A;Molecule type: DNA
 A;Residues: 1-5 <AND>
 A;Cross-references: CB:J03371; NID:G152455; PIDN:RAD15030.1; PID:G4262874

Query Match 34.6%; Score 9; DB 2; Length 5;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDNFS 5
 | |
 Db 1 MDTNS 5

RESULT 5
 A32516
 Cholecystokinin-5 - dog
 N;Alternate names: CCK-5
 C;Species: Canis lupus familiaris (dog)
 C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
 C;Accession: A32516
 R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
 Am. J. Physiol. 252, G272-G275, 1987
 A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest
 A;Reference number: A32516; MUID:87153871; PMID:3826354
 A;Accession: A32516
 A;Molecule type: protein
 A;Residues: 1-5 <SHI>
 A;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto
 C;Superfamily: gastrin
 C;Keywords: amidated carboxyl end; neuropeptide
 F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 30.8%; Score 8; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LD 2
 |
 Db 3 MD 4

RESULT 6
 S70615
 endo-1,4-beta-xylanase (EC 3.2.1.8) - Streptomyces sp. (Chainia sp. NCL 82.5.1) (fragment)
 N;Alternate names: xylanase
 C;Species: Streptomyces sp.
 A;Variety: Chainia sp. NCL 82.5.1
 C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C;Accession: S70615
 R;Rao, M.; Khadilkar, S.; Bandivadekar, K.R.; Deshpande, V.
 Biochem. J. 316, 771-775, 1996
 A;Title: Structural environment of an essential cysteine residue of xylanase from Chain:
 A;Reference number: S70615; MUID:96265041; PMID:8670151
 A;Accession: S70615
 A;Molecule type: protein
 A;Residues: 1-5 <RAO>
 A;Experimental source: Chainia sp. strain NCL 82.5.1
 A;Note: the source is designated as Chainia sp.
 C;Function:
 A;Description: endohydrolyzation of beta-1,4-xylosidic linkages in xylans
 A;Pathway: fermentation of hemicellulose into ethanol
 C;Keywords: glycosidase; hydrolase

Query Match 30.8%; Score 8; DB 2; Length 5;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DNF 4
 |
 Db 1 ETF 3

RESULT 7
 PT0644
 T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C;Accession: PT0644
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Accession: PT0644
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEE>
 A;Cross-references: UNIPROT:Q9Z2T6
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 30.8%; Score 8; DB 2; Length 5;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
 | |
 Db 3 SFT 5

RESULT 8
 D60274
 major protein antigen MPT46 - Mycobacterium tuberculosis (fragment)
 C;Species: Mycobacterium tuberculosis
 C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C;Accession: D60274
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.

Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture
A;Reference number: A60274; MUID:9109989; PMID:1898899
A;Accession: D60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>

Query Match 26.9%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3

Db 2 DS 3

RESULT 9

T-cell receptor beta chain V-D-J region - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0679

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-5 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J

A;Accession: PT0708

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-5 <FEE>

A;Experimental source: newborn thymus, strain BALB/c, 161-2B

C;Keywords: T-cell receptor

Query Match 26.9%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3

Db 4 DD 5

RESULT 10

A44692

fulicin - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C;Accession: A44692

R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; No

Biochem. Biophys. Res. Commun. 178, 486-493, 1991

A;Title: Fulicin, a novel neuropeptide containing a D-amino acid residue isolated from b

A;Reference number: A44692; MUID:91315471; PMID:1859408

A;Accession: A44692

A;Molecule type: protein

A;Residues: 1-5 <OHT>

A;Cross-references: UNIPROT:P35905

C;Keywords: amidated carboxyl end; D-amino acid; neuropeptide

F;2/Modified site: D-asparagine (Asn) #status experimental

F;5/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 26.9%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FS 5

Db 1 FN 2

RESULT 11

PT0600

T-cell receptor beta chain V-D-J region (120-1C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C;Accession: PT0600

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0600

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Cross-references: UNIPROT:Q9D4H2; UNIPROT:Q8BGT7

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 26.9%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3

Db 4 DS 5

RESULT 12

PT0601

T-cell receptor beta chain V-D-J region (120-2K) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004

C;Accession: PT0601; PT0617; PT0694

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0601

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Cross-references: UNIPROT:Q64512

A;Experimental source: newborn thymus, strain BALB/c, clone 120-2K

A;Accession: PT0617

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FE3>

A;Experimental source: newborn thymus, strain BALB/c, 120-2CA

A;Accession: PT0694

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-5 <FE2>

A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1H

C;Keywords: T-cell receptor

Query Match 26.9%; Score 7; DB 2; Length 5;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3

Db 4 DD 5

RESULT 13

A26830

mitosis inhibiting peptide - mouse

C;Species: Mus musculus (house mouse)

C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C;Accession: A26830

R;Reichelt, K.; Elgjo, K.; Edminson, P.D.

Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987
 A;Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.
 A;Reference number: A26830; MUID:87298602; PMID:3619940
 A;Accession: A26830

A;Molecule type: protein
 A;Residues: 1-5 <REI>
 A;Superfamily: unassigned animal peptides
 C;Keywords: blocked amino end; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.9%; Score 7; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DN 3
 |
 Db 3 DS 4

RESULT 14

A44955
 alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - Vibrio harveyi (fragment)

C;Species: Vibrio harveyi
 C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
 C;Accession: A44955
 R;Paquette, O.; Tu, S.C.
 Photochem. Photobiol. 50, 817-825, 1989

A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib
 A;Reference number: A44955; MUID:90175700; PMID:2626493
 A;Accession: A44955
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <PAQ>
 C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase

Query Match 23.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
 |
 Db 1 F 1

RESULT 15

B60274
 major protein antigen MPT32 - Mycobacterium tuberculosis (fragment)

C;Species: Mycobacterium tuberculosis
 C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
 C;Accession: B60274
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
 Infect. Immun. 59, 372-382, 1991

A;Title: Isolation and partial characterization of major protein antigens in the culture
 A;Reference number: A60274; MUID:91099989; PMID:1898899
 A;Accession: B60274
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-5 <NAG>

Query Match 23.1%; Score 6; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 D 2
 |
 Db 1 D 1

Search completed: September 10, 2005, 01:15:41
 Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 00:57:03 ; Search time 166 Seconds
(without alignments)
15.424 Million cell updates/sec

Title: US-10-795-795-12
Perfect score: 26
Sequence: 1 LDNFS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 27

Minimum DB seq length: 5
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	42.3	5	1 RE11_LITRU	P82070 litoria rub
2	8	30.8	5	1 RE21_LITRU	P82071 litoria rub
3	8	30.8	5	1 RE31_LITRU	P82072 litoria rub
4	7	26.9	5	1 AL14_CARMA	P81817 carcinus ma
5	7	26.9	5	1 B10A_CITFR	P13071 citrobacter
6	7	26.9	5	1 RE32_LITRU	P82073 litoria rub
7	7	26.9	5	1 TP1S_CANFA	P54714 canis fami
8	7	26.9	5	1 UXA4_CHLTR	P38005 chlamydia t
9	6	23.1	5	1 E103_LITRU	P82099 litoria rub
10	6	23.1	5	1 E104_LITRU	P82100 litoria rub
11	6	23.1	5	1 FARP_ARTTR	P41853 artiposthi
12	6	23.1	5	1 FARP_CHICK	P83308 gallus gall
13	6	23.1	5	1 MPA4_JUNVI	P81826 juniperus v
14	6	23.1	5	1 PAP2_PARMA	P81864 pardachirus
15	6	23.1	5	1 SUGA_ACHDO	P19991 acheta dome
16	6	23.1	5	1 TRM3_ECOLI	P13973 escherichia
17	6	23.1	5	1 UC22_MAIZE	P80628 zea mays (m
18	6	23.1	5	2 Q99007	Q99007 hordeum vul
19	6	23.1	5	2 P83073	P83073 bacillus ce
20	4	15.4	5	1 AP21_EISFO	P84182 eisenia foe
21	4	15.4	5	1 B10B_CITFR	P12997 citrobacter
22	4	15.4	5	1 PRCT_CARMA	P67857 carcinus ma
23	4	15.4	5	1 PRCT_LIMPO	P67858 limulus pol
24	4	15.4	5	1 PRCT_PERAM	P67859 periplaneta
25	4	15.4	5	1 PSK_DAUCA	P58261 daucus caro
26	2	7.7	5	1 BPP7_BOTIN	P30425 bothrops in
27	2	7.7	5	1 UF01_MOUSE	P38639 mus musculu

ALIGNMENTS

RESULT 1
RE11_LITRU
ID RE11_LITRU STANDARD; PRT; 5 AA.
AC P82070;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -|- FUNCTION: Shows neither neuropeptide activity nor antibiotic
activity.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -|- MASS SPECTROMETRY: MW=598; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match 42.3%; Score 11; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 LDNFS 5
DB 1 VDFFA 5

RESULT 2

RE21_LITRU
ID RE21_LITRU STANDARD; PRT; 5 AA.
AC P82071;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylinae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -|- FUNCTION: Shows neither neuropeptide activity nor antibiotic
activity.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -|- MASS SPECTROMETRY: MW=626; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9C9CB10300000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 20.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNFS 5
: :
Db 1 IEFFA 5

RESULT 3
RE31_LITRU
ID RE31_LITRU STANDARD; PRT; 5 AA.
AC P82072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
[1]
RN SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RC Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=655; METHOD=FAB; RANGE=1-5; NOTE=Ref.1.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 5 5
FT SEQUENCE 5 AA; 656 MW; 71A9C9CB1030000 CRC64;

Query Match 30.8%; Score 8; DB 1; Length 5;
Best Local Similarity 20.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDNFS 5
: :
Db 1 IEFFT 5

RESULT 4
AL14_CARMA
ID AL14_CARMA STANDARD; PRT; 5 AA.
AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
[1]
RN SEQUENCE.
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RC MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
CC Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD RES 5 5
FT SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FS 5
: :
Db 1 YS 2

RESULT 5
BIOA_CITFR
ID BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
DN Name=bioA;
GN Citrobacter freundii.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=89006280; PubMed=2971595; DOI=10.1016/0378-1119(88)90397-6;
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RT Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-diaminononanoate.
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent aminotransferase family.

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EMBL; M21922; -; NOT_ANNOTATED_CDS.

DR PIR; I40697; I40697.
DR InterPro; IPR005814; Aminotrans_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Aminotransferase; Biotin biosynthesis; Pyridoxal phosphate;
KW Transferase.
FT NON_TER 5 5
FT SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3
: :
Db 4 DD 5

RESULT 6
RE32_LITRU
ID RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- FUNCTION: Shows neither neuropeptide activity nor antibiotic
activity.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
KW Amphibian defense peptide; Direct protein sequencing.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 FS 5
|:
DB 4 FT 5

RESULT 7
TPIS CANFA
ID TPIS CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate
isomerase) (Fragment).
GN Name=TP11;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -|- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
phosphate.
CC -|- PATHWAY: Plays an important role in several metabolic pathways.
CC -|- SUBUNIT: Homodimer (By similarity).
CC -|- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro; IPR000652; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Direct protein sequencing; Fatty acid biosynthesis; Gluconeogenesis;
KW Glycolysis; Isomerase; Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3
|:
DB 1 P 1

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5 5 Methionine amide.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
|:
DB 1 P 1

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5 5 Methionine amide.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
|:
DB 1 P 1

Db 4 NN 5

RESULT 8
UXA4 CHLTR STANDARD; PRT; 5 AA.
ID UXA4 CHLTR
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Megi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christian G., Birkelund S., Vreton E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 4.5, its MW is: 28 kDa.
CC Siena-2DPAGE; P38005; --
DR Direct protein sequencing.
KW NON_TER 5 5
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865A8000000 CRC64;

Query Match 26.9%; Score 7; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DN 3
|:
DB 4 DS 5

RESULT 9
EI03 LITRU STANDARD; PRT; 5 AA.
ID EI03 LITRU
AC P82059;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 5 5 Methionine amide.
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
|:
DB 1 P 1

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RESULT 10
EIO4_LITRU
ID EIO4_LITRU STANDARD; PRT; 5 AA.
AC P82100;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Electrin 4.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -|- SUBCELLULAR LOCATION: Secreted.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD RES 5 Histidine amide.
SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
Db 1 F 1

RESULT 11
FARP_ARTTR
ID FARP_ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide RYIRP-amide.
OS Artiposchia triangulata (New Zealand flatworm).
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Terricola; Geoplanidae; Arthurdendyus.
OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; PubMed=7909164; DOI=10.1016/0167-0115(94)90189-9;
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYIRPamide: a turbellarian FMRamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994).
CC -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 5 Phenylalanine amide.
SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
Db 5 F 5

RESULT 12
FARP_CHICK
ID FARP_CHICK STANDARD; PRT; 5 AA.
AC P83308;

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DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide (LPLRF-amide).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RX PubMed=6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRamide.";
RL Nature 305:328-330(1983).
CC -|- FUNCTION: May function as a neurotransmitter or modulator.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
CC family.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 5 Phenylalanine amide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 F 4
Db 5 F 5

RESULT 13
MPA4_JUNVI
ID MPA4_JUNVI STANDARD; PRT; 5 AA.
AC P81826;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Major pollen allergen Jun v 4 (Fragment).
OS Juniperus virginiana (Eastern red cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
OX NCBI_TaxID=39584;
RN [1]
RP SEQUENCE, AND ALLERGENIC PROPERTIES.
RC TISSUE=Pollen;
RX MEDLINE=21315424; PubMed=11422137;
RA Miodoro-Horluti T., Goldblum R.M., Brooks E.G.;
RT "Identification of mutations in the genes for the pollen allergens of
RT eastern red cedar (Juniperus virginiana).";
RL Clin. Exp. Allergy 31:771-778(2001).
CC -|- ALLERGEN: Causes an allergic reaction in human. Binds to IgE of
CC patients who are allergic to J.ashei.
KW Allergen; Direct protein sequencing.
FT NON TER 5
SQ SEQUENCE 5 AA; 491 MW; 75B33DDAADB00000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 D 2
Db 2 D 2

RESULT 14
PAP2_PARMA
ID PAP2_PARMA STANDARD; PRT; 5 AA.

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Search completed: September 10, 2005, 01:14:56
Job time : 168 secs

AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mores sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mores sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels in
CC membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pardaxin family.
KW Direct protein sequencing; Toxin.
FT NON_TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
Db 2 F 2

RESULT 15
SUGA_ACHDO STANDARD; PRT; 5 AA.
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Suboesophageal ganglion pentapeptide.
OS Acheta domesticus (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]
RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the suboesophageal
RT ganglion of Acheta domesticus (Orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -!- SUBCELLULAR LOCATION: Main peptide from the suboesophageal
CC ganglia.
DR PIR; JS0319.
KW Direct protein sequencing.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 23.1%; Score 6; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 F 4
Db 5 F 5

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2005, 01:08:05 ; Search time 41 Seconds
(without alignments)
9.104 Million cell updates/sec

Title: US-10-795-795-12

Perfect score: 26

Sequence: 1 LONFS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 15555

Minimum DB seq length: 5

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	5	4	US-09-911-129B-12
2	17	65.4	5	4	US-09-788-006-163
3	16	61.5	5	1	US-08-385-443-4
4	16	61.5	5	1	US-08-302-829-7
5	16	61.5	5	1	US-08-481-840A-5
6	16	61.5	5	1	US-08-403-718-7
7	16	61.5	5	1	US-08-619-462-7
8	16	61.5	5	2	US-08-667-001-21
9	16	61.5	5	2	US-08-441-871-146
10	16	61.5	5	2	US-08-705-660-37
11	16	61.5	5	3	US-09-082-837A-7
12	16	61.5	5	3	US-08-989-045-37
13	16	61.5	5	3	US-08-591-632-20
14	16	61.5	5	3	US-08-591-632-31
15	16	61.5	5	3	US-09-421-845-7
16	16	61.5	5	3	US-09-187-859-242
17	16	61.5	5	3	US-09-187-859-1725
18	16	61.5	5	3	US-09-611-451-20
19	16	61.5	5	3	US-09-611-451-31
20	16	61.5	5	4	US-09-839-542B-242
21	16	61.5	5	4	US-09-839-542B-1725
22	16	61.5	5	4	US-09-315-355A-37
23	16	61.5	5	4	US-09-788-006-161
24	16	61.5	5	4	US-09-788-006-162
25	15	57.7	5	3	US-09-171-945-29
26	15	57.7	5	3	US-09-187-859-323
27	15	57.7	5	3	US-09-187-859-2134

28 15 57.7 5 4 US-09-839-542B-323 Sequence 323, App
29 15 57.7 5 4 US-09-839-542B-2134 Sequence 2134, App
30 14 53.8 5 1 US-08-325-509-51 Sequence 51, Appl
31 14 53.8 5 1 US-08-446-486-11 Sequence 11, Appl
32 14 53.8 5 1 US-08-340-045-1 Sequence 1, Appl
33 14 53.8 5 1 US-08-290-448A-1 Sequence 1, Appl
34 14 53.8 5 1 US-08-290-448A-1 Sequence 1, Appl
35 14 53.8 5 1 US-08-463-308-11 Sequence 11, Appl
36 14 53.8 5 1 US-08-175-069A-1 Sequence 1, Appl
37 14 53.8 5 2 US-08-691-997-1 Sequence 1, Appl
38 14 53.8 5 3 US-08-871-302A-1 Sequence 1, Appl
39 14 53.8 5 3 US-08-461-939B-1 Sequence 1, Appl
40 14 53.8 5 3 US-08-461-000-1 Sequence 1, Appl
41 14 53.8 5 3 US-09-187-859-322 Sequence 322, App
42 14 53.8 5 4 US-09-839-542B-322 Sequence 322, App
43 14 53.8 5 5 PCT-US94-03744-7 Patent No. 5254799
44 14 53.8 5 6 5254799-13 Patent No. 5254799
45 14 53.8 5 6 5254799-13 Patent No. 5254799

ALIGNMENTS

RESULT 1
US-09-911-129B-12
; Sequence 12, Application US/09911129B
; Patent No. 6703364
; GENERAL INFORMATION:
; APPLICANT: Cleveland State University
; APPLICANT: Kalafatis, Michael
; APPLICANT: Mann, Kenneth G.
; TITLE OF INVENTION: Thrombin Generation Inhibitor
; FILE REFERENCE: 27433/04004
; CURRENT APPLICATION NUMBER: US/09/911,129B
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-129B-12

Query Match 100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LONFS 5
Db 1 LONFS 5

RESULT 2
US-09-788-006-163
; Sequence 163, Application US/09788006
; Patent No. 6832162
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 163
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-788-006-163

Query Match 65.4%; Score 17; DB 4; Length 5;

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Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDNFS 5
   ||| :
Db 1 LDNIA 5

RESULT 3
US-08-385-443-4
; Sequence 4, Application US/08385443
; Patent No. 5534495
; GENERAL INFORMATION:
; APPLICANT: PERT, CANDANCE B.
; APPLICANT: RUFF, MICHAEL R.
; TITLE OF INVENTION: TREATMENT OF NON-HIV NEUROPATHIC
; TITLE OF INVENTION: PAIN SYNDROMES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JULES E. GOLDBERG
; STREET: 261 MADISON AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/385,443
; FILING DATE: 08-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/067,523
; FILING DATE: 23-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDBERG, JULES E.
; REGISTRATION NUMBER: 24,408
; REFERENCE/DOCKET NUMBER: ADVANCED PEPTIDES P5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-986-4090
; TELEFAX: 212-818-9479
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-385-443-4

Query Match 61.5%; Score 16; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
   ||| :
Db 2 DNYT 5

RESULT 4
US-08-302-829-7
; Sequence 7, Application US/08302829
; Patent No. 5756449
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Anders J
; APPLICANT: ASTON, Roger
; APPLICANT: CARLEN, Peter L
; APPLICANT: DOOB, Penelope R
; APPLICANT: MacFADDEN, Douglas K
; APPLICANT: PHIPPS, David J

US-08-302-829-7

Query Match 61.5%; Score 16; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
   ||| :
Db 2 DNYT 5

RESULT 5
US-08-481-840A-5
; Sequence 5, Application US/08481840A
; Patent No. 5763406
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Ove
; APPLICANT: MacFADDEN, D.
; TITLE OF INVENTION: Peptides for Treatment
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive

US-08-302-829-7

Query Match 61.5%; Score 16; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNFS 5
   ||| :
Db 2 DNYT 5

RESULT 5
US-08-481-840A-5
; Sequence 5, Application US/08481840A
; Patent No. 5763406
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, Ove
; APPLICANT: MacFADDEN, D.
; TITLE OF INVENTION: Peptides for Treatment
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive
```


CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk, 3.50 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,840A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,777
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Iwanicki, John P
REGISTRATION NUMBER: 34,628
REFERENCE/DOCKET NUMBER: 93,741-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: peptide
US-08-481-840A-5

Query Match 61.5%; Score 16; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
DB 2 DNYT 5

RESULT 6
US-08-403-718-7
Sequence 7, Application US/08403718
Patent No. 5795858
GENERAL INFORMATION:
APPLICANT: MICHAELIS, JURGEN
APPLICANT: SLEIGH, MERILYN J.
TITLE OF INVENTION: TREATMENT OR PREVENTION OF CROHN'S
DISEASE AND/OR ULCERATIVE COLITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,718
FILING DATE: 31-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-74
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000

TELEFAX: (704) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-403-718-7

Query Match 61.5%; Score 16; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
DB 2 DNYT 5

RESULT 7
US-08-619-462-7
Sequence 7, Application US/08619462
Patent No. 5798335
GENERAL INFORMATION:
APPLICANT: MICHAELIS, JURGEN
APPLICANT: Trigg, Timothy Elliot
TITLE OF INVENTION: METHOD FOR THE TREATMENT OR PREVENTION OF
ECZEMA/DERMATITIS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,462
FILING DATE: 07-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MITCHARD, LEONARD C.
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 47-84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (704) 816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-619-462-7

Query Match 61.5%; Score 16; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
DB 2 DNYT 5

RESULT 8
US-08-667-001-21
Sequence 21, Application US/08667001

; Patent No. 5827827
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D.
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,001
; FILING DATE: 20-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/335,039
; FILING DATE: 16-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lewis, Donald G.
; REGISTRATION NUMBER: 28,636
; REFERENCE/DOCKET NUMBER: TSRI 282.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2937
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1
; OTHER INFORMATION: /note= "sequence = Pl-Pn of formula
; OTHER INFORMATION:
US-08-667-001-21

Query Match 61.5%; Score 16; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 2 NFS 4

RESULT 9

US-08-441-871-146
; Sequence 146, Application US/08441871
; Patent No. 5846765
; GENERAL INFORMATION:
; APPLICANT: Matthews, David J.
; APPLICANT: Wells, James A.
; APPLICANT: Zollner, Mark J.
; TITLE OF INVENTION: Identification of No. 5846765el Substrates
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,871
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/418928
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/161692
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/864452
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/09133
; FILING DATE: 03-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/743614
; FILING DATE: 09-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715300
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/683400
; FILING DATE: 10-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/621667
; FILING DATE: 03-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Daryl B.
; REGISTRATION NUMBER: 32,637
; REFERENCE/DOCKET NUMBER: 645P5C2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1249
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-441-871-146

Query Match 61.5%; Score 16; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 2 NFS 4

RESULT 10

US-08-705-660-37
; Sequence 37, Application US/08705660
; Patent No. 5858683
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA

;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/705,660
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GREENHALGH, DUNCAN A
;; REGISTRATION NUMBER: 38,678
;; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 37:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-705-660-37

Query Match 61.5%; Score 16; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDN 3
Db 1 LDN 3

RESULT 11
US-09-082-837A-7
; Sequence 7, Application US/09082837A
; Patent No. 6011014
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Anders J
; APPLICANT: ASTON, Roger
; APPLICANT: CARLEN, Peter L
; APPLICANT: DOOB, Penelope R
; APPLICANT: MACFADDAEN, Douglas K
; APPLICANT: PHIPPS, David J
; APPLICANT: RATHJEN, Deborah
; APPLICANT: WIDMER, Fred
; TITLE OF INVENTION: Peptide T and Related Peptides in the Treatment of
; TITLE OF INVENTION: Inflammation, Including Multiple sclerosis
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BANNER & WITCOFF, LTD.
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,837A
; FILING DATE: 21-JUN-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,829
; FILING DATE: 29-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00649
; FILING DATE: 29-MAR-1993

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/987,674
;; FILING DATE: 09-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/915,118
;; FILING DATE: 17-JUL-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DK 645/92
;; FILING DATE: 14-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/858,832
;; FILING DATE: 27-MAR-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Drenkoff, W. Dennis
;; REGISTRATION NUMBER: 27193
;; REFERENCE/DOCKET NUMBER: 94,772-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-715-1000
;; TELEFAX: 312-715-1234
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: both
;; MOLECULE TYPE: peptide
US-09-082-837A-7

Query Match 61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNFS 5
Db 2 DNYT 5

RESULT 12
US-08-989-045-37
; Sequence 37, Application US/08989045
; Patent No. 6027905
; GENERAL INFORMATION:
; APPLICANT: KEESEE, SUSAN
; APPLICANT: OBAR, ROBERT
; APPLICANT: WU, YING-JYE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL CANCER
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,045
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GREENHALGH, DUNCAN A
; REGISTRATION NUMBER: 38,678
; REFERENCE/DOCKET NUMBER: MTP-023 (8395/27)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-989-045-37

Query Match 61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDN 3
Db 1 LDN 3

DNAR = P2

RESULT 13
US-08-591-632-20
; Sequence 20, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-20

Query Match 61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 1 NFS 3

RESULT 14
US-08-591-632-31
; Sequence 31, Application US/08591632
; Patent No. 6261558
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos F.
; APPLICANT: Burton, Dennis R.
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,632
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/11907
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/308,841
; FILING DATE: 19-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,619
; FILING DATE: 26-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,409
; FILING DATE: 19-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 332.3
; TELEPHONE: (619) 784-2937
; TELEFAX: (619) 784-9399
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-632-31

Query Match 61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NFS 5
Db 1 NFS 3

RESULT 15
US-09-421-845-7
; Sequence 7, Application US/09421845
; Patent No. 6265374

```
; GENERAL INFORMATION:
; APPLICANT: Jorgensen
; APPLICANT: Aston
; APPLICANT: Carlen
; APPLICANT: Doob
; APPLICANT: MacFadden
; APPLICANT: Phipps
; APPLICANT: Rathjen
; APPLICANT: Widmer
; TITLE OF INVENTION: Peptide T and Related Peptides In the Treatment of
; FILE OF INVENTION: Inflammation, Including Multiple Sclerosis.
; FILE REFERENCE: Peptide T Inflammation
; CURRENT APPLICATION NUMBER: US/09/421,845
; CURRENT FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/082,837
; PRIOR FILING DATE: 1998-05-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-421-845-7

Query Match      61.5%; Score 16; DB 3; Length 5;
Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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Qy      2 DNFS 5
        ||::
Db      2 DNYT 5
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Search completed: September 10, 2005, 01:16:29
Job time : 42 secs

11-1-04-0

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